

MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: No
US-08-946-525-4

Query Match 36.6%; Score 26; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPG 10
| | | |
Db 2 HIGPG 6

RESULT 27

US-09-082-279B-920
Sequence 920, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Arwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-920

Query Match 36.6%; Score 26; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
| | | |
Db 1 YGPGW 5

RESULT 28

US-09-315-304B-920
Sequence 920, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Arwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide

US-09-315-304B-920

Query Match 36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
| | | |
Db 1 YGPGW 5

RESULT 29

US-09-599-286-4
Sequence 4, Application US/09599286
Patent No. 6447778
GENERAL INFORMATION:
APPLICANT: Arye Rubinstein, Barry R. Bloom, Yair Devash and Stanley J.
Cryz
TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND
PREVENTION OF HIV
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Ebenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,286
FILING DATE: 22-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/946,525
FILING DATE: October 7, 1997
APPLICATION NUMBER: 08/785,696
FILING DATE: January 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: peptide
HYPOTHETICAL: No
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-599-286-4

Query Match 36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPG 10
| | | |
Db 2 HIGPG 6

RESULT 30

US-09-834-784-920

```

; Sequence 920, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-920

```

```

Query Match      36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 YGPGW 11
   |||
Db 1 YGKGW 5

```

```

RESULT 31
US-09-515-965A-920
; Sequence 920, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sistr, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-920

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```

Query Match      36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 YGPGW 11
   |||
Db 1 YGKGW 5

```

RESULT 32

```

US-09-350-641C-920
; Sequence 920, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-920

```

```

Query Match      36.6%; Score 26; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 YGPGW 11
   |||
Db 1 YGKGW 5

```

```

RESULT 33
US-08-250-789A-94
; Sequence 94, Application US/08250789A
; Patent No. 5635597
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Chernov-Rogan, Tania
; APPLICANT: Davis, Ann M.
; TITLE OF INVENTION: Peptides That Bind to IL-2 Receptors
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,789A
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5635597v1e1, Vernon A.
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-57/1043
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids

```

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-250-789A-94

Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGPG 10
|||
Db 2 YGPG 5

RESULT 34

US-08-341-219-15
Sequence 15, Application US/08341219
Patent No. 5643877
GENERAL INFORMATION:
APPLICANT: Zohar, Y.
APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Sherwood, N.
APPLICANT: Gotthilf, Y.
TITLE OF INVENTION: Compounds and Methods For Controlling
TITLE OF INVENTION: Reproduction in Fish
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,219
FILING DATE: 05-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 8399-003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= Glu1
OTHER INFORMATION: /note= "pyroglutamic acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= Gly10
OTHER INFORMATION: /note= "amidated"
US-08-341-219-15

Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
:|:|
Db 1 EHWMSGW 7

RESULT 35

US-08-341-219-16
Sequence 16, Application US/08341219
Patent No. 5643877
GENERAL INFORMATION:
APPLICANT: Zohar, Y.
APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Sherwood, N.
APPLICANT: Gotthilf, Y.
TITLE OF INVENTION: Compounds and Methods For Controlling
TITLE OF INVENTION: Reproduction in Fish
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,219
FILING DATE: 05-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 8399-003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= Glu1
OTHER INFORMATION: /note= "pyroglutamic acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /label= Gly10
OTHER INFORMATION: /note= "amidated"
US-08-341-219-16
Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
: : :
Db 1 EHWSHGW 7

RESULT 36

US-08-253-030-23
; Sequence 23, Application US/08253030
; Patent No. 5712373

GENERAL INFORMATION:

APPLICANT: EDA, Yasuyuki
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: MATSUSHITA, Shuzo
APPLICANT: HATTORI, Toshio
APPLICANT: TAKATSUKI, Kiyoshi
TITLE OF INVENTION: HIV Monoclonal Antibody
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,030
FILING DATE: 02-JUN-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/723,916
FILING DATE: 01-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 175075/1990
FILING DATE: 02-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 188300/1990
FILING DATE: 16-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 74129/215/AOPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-253-030-23

Query Match

Best Local Similarity 36.6%; Score 26; DB 1; Length 10;
Matches 4; Conservativity 0; Pred. No. 3.1e+02;
Indels 1; Gaps 0;

QY 6 HYPG 10
: : :
Db 1 HIGPG 5

RESULT 37

US-08-253-030-25
; Sequence 25, Application US/08253030
; Patent No. 5712373

GENERAL INFORMATION:

APPLICANT: EDA, Yasuyuki
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: MATSUSHITA, Shuzo
APPLICANT: HATTORI, Toshio
APPLICANT: TAKATSUKI, Kiyoshi
TITLE OF INVENTION: HIV Monoclonal Antibody
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,030
FILING DATE: 02-JUN-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/723,916
FILING DATE: 01-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 175075/1990
FILING DATE: 02-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 188300/1990
FILING DATE: 16-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 74129/215/AOPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-253-030-25

Query Match

Best Local Similarity 36.6%; Score 26; DB 1; Length 10;
Matches 4; Conservativity 0; Pred. No. 3.1e+02;
Indels 1; Gaps 0;

QY 6 HYPG 10
: : :
Db 2 HIGPG 6

RESULT 38

US-08-425-069-19
; Sequence 19, Application US/08425069
; Patent No. 5728810

GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hirman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: 301 No. 5728810th Washington Street
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22046
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/425,069
 FILING DATE: 19-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1447-106P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 TELEX:
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Araneus gemmoides
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..10
 OTHER INFORMATION: /label= fragment
 OTHER INFORMATION: /note="fragment of sequence from Araneus dragline"
 OTHER INFORMATION: silk protein."
 US-08-425-069-19

Query Match 36.6%; Score 26; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGPG 10
 ||||
 Db 3 YGPG 6
 RESULT 39
 US-08-687-559-10
 ; Sequence 10, Application US/08687559
 ; Patent No. 5955647
 ; GENERAL INFORMATION:
 ; APPLICANT: Fitcher, John H.
 ; APPLICANT: Beachy, Roger N.
 ; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
 ; TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/687,559

FILING DATE: No. 5955647ember 18, 1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/01467
 FILING DATE: 03-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Learn, June M.
 REGISTRATION NUMBER: 31,238
 REFERENCE/DOCKET NUMBER: 07302/011001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-678-5070
 TELEFAX: 619-678-5099
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-687-559-10

Query Match 36.6%; Score 26; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10
 ||||
 Db 3 HIGPG 7

RESULT 40
 US-08-317-844B-19
 ; Sequence 19, Application US/08317844B
 ; Patent No. 5989894
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, Randolph V.
 ; APPLICANT: Xu, Ming
 ; APPLICANT: Himm, Michael B.
 ; TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
 ; TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch
 ; STREET: 301 No. 5989894th Washington Street
 ; CITY: Falls Church
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22046
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/317,844B
 ; FILING DATE: 04-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murphy Jr., Gerald M
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 1447-105P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 241-1300
 ; TELEFAX: (703) 241-2848
 ; TELEX: 248345
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:

ORGANISM: Araneus gemmoides
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..10
OTHER INFORMATION: /label= fragment
OTHER INFORMATION: /note= "fragment of sequence from Araneus dragline"
OTHER INFORMATION: silk protein."
US-08-317-844B-19

Query Match 36.6%; Score 26; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 YGPG 10
| | | |
DB 3 YGPG 6

RESULT 41
US-08-946-525-15
Sequence 15, Application US/08946525
Patent No. 6139843

GENERAL INFORMATION:

APPLICANT: Arye Rubinstein, Barry R. Bloom, Yair Devash and Stanley J. Cryz
TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND
PREVENTION OF HIV
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amster, Roststein & Ebenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,525
FILING DATE: October 7, 1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/785,696
FILING DATE: January 17, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Bogosian, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/448

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 10
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: peptide
HYPOTHETICAL: NO
US-08-946-525-15

Query Match 36.6%; Score 26; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 HYGP 10
| | | |
DB 2 HIGP 6

RESULT 42

US-08-912-314A-15
Sequence 15, Application US/08912314A
Patent No. 6210927

GENERAL INFORMATION:

APPLICANT: Zohar, Y.
APPLICANT: Rivier, J.
APPLICANT: Powell, J.

APPLICANT: Sherwood, N.
APPLICANT: Gochilif, Y.

TITLE OF INVENTION: Compounds and Methods For Controlling
Reproduction in Fish

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/912,314A
FILING DATE: 30-JUN-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/341,219
FILING DATE: 05-DEC-1994
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 8399-003-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: Modified-site

LOCATION: 1
OTHER INFORMATION: /product= "OTHER"

OTHER INFORMATION: /label= Glu1
OTHER INFORMATION: /note= "pyroglutamic acid"

NAME/KEY: Modified-site

LOCATION: 10
OTHER INFORMATION: /product= "OTHER"

OTHER INFORMATION: /label= Gly10
OTHER INFORMATION: /note= "amidated"

US-08-912-314A-15

Query Match 36.6%; Score 26; DB 3; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYGPW 11
| | | |
DB 1 EHMHWG 7

RESULT 43

US-08-912-314A-16
; Sequence 16, Application US/08912314A
; Patent No. 6210927
; GENERAL INFORMATION:
; APPLICANT: Zohar, Y.
; APPLICANT: Rivier, J.
; APPLICANT: Powell, J.
; APPLICANT: Sherwood, N.
; APPLICANT: Gethilf, Y.
; TITLE OF INVENTION: Compounds and Methods For Controlling
; TITLE OF INVENTION: Reproduction in Fish
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,314A
; FILING DATE: 30-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/341,219
; FILING DATE: 05-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 8399-003-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Glu1
; OTHER INFORMATION: /note= "pyroglutamic acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Gly10
; OTHER INFORMATION: /note= "amidated"
US-08-912-314A-16
Query Match 36.6%; Score 26; DB 3; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 KHYGPGW 11
; : : :
; : : :
Db 1 EHWSHGW 7
RESULT 44
US-09-599-286-15
; Sequence 15, Application US/09599286

; Patent No. 6447778
; GENERAL INFORMATION:
; APPLICANT: Arye Rubinstein, Barry R. Bloom, Yair Devash and Stanley J.
; CITY2
; TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND
; PREVENTION OF HIV
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amster, Rothstein & Ebenstein
; STREET: 90 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/599,286
; FILING DATE: 22-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,525
; FILING DATE: October 7, 1997
; APPLICATION NUMBER: 08/785,686
; FILING DATE: January 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Elizabeth A
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: 96700/448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: peptide
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-599-286-15
Query Match 36.6%; Score 26; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 HYGPG 10
; : : :
; : : :
Db 2 HIGPG 6
RESULT 45
US-09-401-415-10
; Sequence 10, Application US/09401415
; Patent No. 6503732
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
; OVERPRODUCE PEPTIDES AND PROTEINS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jupas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/401,415

FILING DATE: 21-Sep-1999

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01467

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bostich, June M.

REGISTRATION NUMBER: 31,238

REFERENCE/DOCKET NUMBER: PD-4074

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..10

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-401-415-10

Query Match

Best Local Similarity 36.6%; Score 26; DB 4; Length 10;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10

Db 3 HYPG 7

Search completed: August 30, 2004, 10:57:15

Job time : 6.34797 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 16.3885 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-5
Perfect score: 71
Sequence: 1 NFKLKHYPGW 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	71	100.0	11	3	AAy69925	Aay69925 Human cyc
2	59	83.1	10	3	AAy69947	Aay69947 Human cyc
3	59	83.1	10	6	ABR84352	AbR84352 Human cyc
4	45	63.4	9	3	AAy69928	Aay69928 Human cyc
5	45	63.4	14	6	ABP74769	Abp74769 Proteome
6	37	52.1	14	2	AAy98453	Aay98453 Alpha D p
7	36	50.7	13	3	AAy98453	Aay98453 Alpha D p
8	32	45.1	14	2	AAy47734	Aay47734 HIV epito
9	32	45.1	14	3	AAy57711	Aay57711 Rat clust
10	31	43.7	8	2	AAW18339	Aaw18339 Bovine p3
11	31	43.7	8	2	AAW18339	Aaw18339 Bovine p3
12	31	43.7	8	2	AAy01990	Aay01990 Tryptic p
13	31	43.7	9	2	AAy31264	Aay31264 HIV princ
14	31	43.7	9	2	AAy31301	Aay31301 Cyclic HI
15	31	43.7	9	2	AAy26700	Aay26700 HIV-PND-p
16	31	43.7	9	2	AAW03401	Aaw03401 HIV princ
17	31	43.7	10	2	AAy31271	Aay31271 HIV princ
18	31	43.7	10	2	AAy31260	Aay31260 HIV princ
19	31	43.7	10	2	AAy31268	Aay31268 HIV princ
20	31	43.7	10	2	AAy31272	Aay31272 HIV princ
21	31	43.7	10	2	AAy31286	Aay31286 HIV princ
22	31	43.7	10	2	AAy30018	Aay30018 HIV cpnd3
23	31	43.7	10	2	AAy31309	Aay31309 Cyclic HI
24	31	43.7	10	2	AAy31293	Aay31293 Cyclic HI
25	31	43.7	10	2	AAy31308	Aay31308 Cyclic HI

26	31	43.7	10	2	AAy31297	Aay31297 Cyclic HI
27	31	43.7	10	2	AAy31305	Aay31305 Cyclic HI
28	31	43.7	10	2	AAy26696	Aay26696 HIV-PND-p
29	31	43.7	10	2	AAy26691	Aay26691 HIV-PND-p
30	31	43.7	10	2	AAy26707	Aay26707 HIV-PND-p
31	31	43.7	10	2	AAy26708	Aay26708 HIV-PND-p
32	31	43.7	10	2	AAy26704	Aay26704 HIV-PND-p
33	31	43.7	11	2	AAy31270	Aay31270 HIV princ
34	31	43.7	11	2	AAy31257	Aay31257 HIV princ
35	31	43.7	11	2	AAy31307	Aay31307 Cyclic HI
36	31	43.7	11	2	AAy31294	Aay31294 Cyclic HI
37	31	43.7	11	2	AAy26692	Aay26692 HIV-PND-p
38	31	43.7	11	2	AAy26706	Aay26706 HIV-PND-p
39	31	43.7	11	2	AAy95759	Aay95759 Alpha-4Be
40	30	42.3	8	5	ABP46859	Abp46859 Human Bly
41	30	42.3	9	1	AAy95363	Aay95363 Variable
42	30	42.3	9	2	AAy31288	Aay31288 HIV princ
43	30	42.3	9	2	AAy30043	Aay30043 HIV princ
44	30	42.3	9	2	AAy26724	Aay26724 HIV-PND-p
45	30	42.3	9	2	AAy26724	Aay26724 HIV-PND-p

ALIGNMENTS

RESULT 1
AAy69925 standard; peptide; 11 AA.
ID AAy69925;
XX
AC
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #5.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO967288-Al.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 50; 64p; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 71; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 NFKLKHYPGW 11
|||||

Db 1 NFKLKHGPGW 11

RESULT 2
AAY69947
ID AAY69947 standard; peptide; 10 AA.
XX
AC AAY69947;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #27.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 56; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;

OY 3 KLKHYGPGW 11
Db 1 KLKHYGPGW 9

Query Match 83.1%; Score 59; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
ABR84352
ID ABR84352 standard; peptide; 10 AA.
XX
AC ABR84352;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CYPB HLA-A2 epitope, SEQ ID NO:3.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A2 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX

PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 7; Page 8; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 10 AA;

OY 3 KLKHYGPGW 11
Db 1 KLKHYGPGW 9

Query Match 83.1%; Score 59; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
AAY69928
ID AAY69928 standard; peptide; 9 AA.
XX
AC AAY69928;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #8.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumors.
XX
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 63.4%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYGPGW 11
|||
1 HYGPGW 6
Db

RESULT 5
ABP74769
ID ABP74769 standard; peptide; 14 AA.
XX
AC ABP74769;
XX
DT 03-FEB-2003 (first entry)
XX
DE Proteome analysis related peptide #54.
XX
KW Proteome analysis; isolation; determination; diagnostic assay; detection;
KW protein marker; identification; metastatic; invasive cancer;
KW differential expression; signalling pathway; chromatography.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277016-A2.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-EP003368.
XX
PR 22-MAR-2001; 2001US-0278171P.
PR 12-SEP-2001; 2001US-0318749P.
PR 20-SEP-2001; 2001US-0323999P.
XX
PA (VLAAS-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Vandekerckhove J, Gevaert K;
XX
DR WPI; 2003-067379/06.
XX
PT Method for isolation of peptides from complex mixture of peptides
PT involves specific chemical and/or enzymatic alteration of at least one
PT type of peptide.
XX
PS Example 20; Page 141; 193pp; English.
XX
CC The present invention describes a method (M1) for the isolation of a
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
CC separating the protein peptide mixture into fractions of peptides via
CC chromatography; (b) chemically, or enzymatically, or chemically and
CC enzymatically, altering at least one amino acid of at least one of the
CC peptides in each fraction, thereby generating a subset of altered
CC peptides; and (c) isolating the altered (flagged) peptides out of each
CC fraction via chromatography, where the chromatography of steps (a) and
CC (c) is performed with the same type of chromatography. M1 can be used for
CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in

CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular
CC changes in cells with physiological changes such as metabolic shift, in
CC the identification of biomarkers in cancers and in the identification of
CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
XX
SQ Sequence 14 AA;

Query Match 63.4%; Score 45; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYGPGW 11
|||
1 HYGPGW 6
Db

RESULT 6
AAR47787
ID AAR47787 standard; protein; 14 AA.
XX
AC AAR47787;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1994 (first entry)
XX
DE HIV epitope #120.
XX
KW HIV-specific; principal neutralisation; epitope; antigen; conjugate;
KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
KW disease; antibody; human; monoclonal antibody; 447 antibody.
XX
OS Human immunodeficiency virus.
XX
PN WO9402626-A1.
XX
PD 03-FEB-1994.
XX
PF 19-JUL-1993; 93WO-US006751.
XX
PR 20-JUL-1992; 92US-00917212.
PR 20-JUL-1992; 92US-00917214.
PR 20-JUL-1992; 92US-00917215.
PR 20-JUL-1992; 92US-00917217.
XX
PA (MERI) MERCK & CO INC.
XX
PI Keller PM, Conley AJ, Shaw AR, Arnold BA;
XX
DR WPI; 1994-048884/06.
XX
PT New conjugates for treating or preventing HIV infection - comprising HIV-
PT specific neutralisation epitopes covalently linked to outer membrane
PT proteosome of Neisseria.
XX
PS Claim 1; Page 151; 181pp; English.
XX
CC The sequences given in AAR47668-788 are HIV-specific selected principal
CC neutralisation epitopes which may be used in an antigenic conjugate
CC linked to purified outer membrane proteosome of Neisseria. This conjugate
CC may be used in an AIDS vaccine which may be used pre- and post-exposure
CC to prevent or treat HIV infection or disease. The vaccine is capable of
CC eliciting specific HIV neutralising antibodies and bind the broadly
CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
CC -2003 to correct PN field.)
XX
SQ Sequence 14 AA;

Query Match 52.1%; Score 37; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 FKLKHYGPG 10
Db 3 YRAAHYGP 11

RESULT 7
AA98453
ID AAY98453 standard; peptide; 13 AA.

AC AAY98453;

DT 31-JUL-2000 (first entry)

DE Alpha D peptide derived from TrkB SEQ ID NO:168.

XX Alpha D peptide; Alpha D region; protein kinase; modulation; activity;
KW cytosolic; anti-diabetic; anorectic; antiinflammatory; dermatological;
KW immunosuppressive; immunomodulator; osteopathic; cardiac; vasotropic;
KW antiarteriosclerotic; protein kinase modulator; cancer; proliferation;
KW restenosis; atherosclerosis; skin disorder; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder; osteoporosis;
KW autoimmune disease; immune disorder; cardiovascular disease.

OS Homo sapiens.

PN WO200018895-A1.

PD 06-APR-2000.

PF 24-SEP-1999; 99WO-US022106.

PR 25-SEP-1998; 98US-00161094.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

PI Ben-Sasson SA;

DR WPI; 2000-328722/28.

PT Peptide derivatives of protein kinase alpha D regions which selectively
modulate the activity of protein kinases.

PS Claim 23; Fig 3; 148pp; English.

XX The present invention describes a peptide derivative (A) of the protein
kinase alpha D region comprising 5-30 amino acids, which modulates the
activity of the protein kinase. AAY98286 to AAY98455 represent peptides
derived from protein kinase alpha D regions, which are used in the
exemplification of the present invention. The peptides have cytosolic,
anti-diabetic, anorectic, antiinflammatory, dermatological, cardiac,
immunosuppressive, immunomodulator, osteopathic, vasotropic and
antiarteriosclerotic activities, and are protein kinase modulators. The
peptides can be used as test peptides to identify protein kinase
modulators. They can also be used to modulate the activity of a protein
kinase in a subject, and in a method of detecting a ligand that binds to
the alpha D region of a protein kinase. They may be used to produce
antibodies that bind to the alpha D region of a protein kinase. The
peptides are useful in the treatment of diseases caused by over- or under
-activity of a protein kinase, e.g. cancer, diseases caused by
proliferation of smooth muscle (e.g. restenosis and atherosclerosis),
skin disorders, diabetes, obesity, diseases of the central nervous
system, inflammatory disorders, autoimmune diseases and other immune
disorders, osteoporosis and cardiovascular diseases

SQ Sequence 13 AA;

Query Match 50.7%; Score 36; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 28;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NFKLKHYGP 9
Db 3 NFKLRAHGP 11

RESULT 8
AAR47734
ID AAR47734 standard; protein; 14 AA.

AC AAR47734;

DT 25-MAR-2003 (revised)

DT 27-JUL-1994 (first entry)

DE HIV epitope #67.

XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;
KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
KW disease; antibody; human; monoclonal antibody; 447 antibody.

OS Human immunodeficiency virus.

PN WO9402626-A1.

PD 03-FEB-1994.

PF 19-JUL-1993; 93WO-US006751.

PR 20-JUL-1992; 92US-00917212.

PR 20-JUL-1992; 92US-00917214.

PR 20-JUL-1992; 92US-00917215.

PR 20-JUL-1992; 92US-00917217.

XX (MERI) MERCK & CO INC.

PI Keller PM, Conley AJ, Shaw AR, Arnold BA;

DR WPI; 1994-048884/06.

PT New conjugates for treating or preventing HIV infection - comprising HIV-
specific neutralisation epitopes covalently linked to outer membrane
proteosome of Neisseria.

PS Claim 1; Page 125; 181pp; English.

XX The sequences given in AAR47668-788 are HIV-specific selected principal
neutralisation epitopes which may be used in an antigenic conjugate
linked to purified outer membrane proteosome of Neisseria. This conjugate
may be used in an AIDS vaccine which may be used pre- and post-exposure
to prevent or treat HIV infection or disease. The vaccine is capable of
eliciting specific HIV neutralising antibodies and bind the broadly
neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
-2003 to correct PN field.)

SQ Sequence 14 AA;

Query Match 45.1%; Score 32; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 KLKHYGP 9
Db 1 KANHYP 7

RESULT 9
AAY57711
ID AAY57711 standard; peptide; 14 AA.

AC AAY57711;

XX

DT 14-MAR-2000 (first entry)
XX
XX Rat clusterin 47 kDa peptide.
DE
XX Clusterin; immunosuppressant; organ rejection; tissue transplantation;
KW autoimmune disease; inflammatory disease; rheumatism; atopy;
KW systemic erythematous; allergy; hay fever.
XX
OS Rattus sp.
XX
XX WO9962541-A1.
XX
XX 09-DEC-1999.
XX
XX 13-MAY-1999; 99WO-JP002474.
XX
XX 01-JUN-1998; 98JP-00151570.
XX
XX (HISM) HISAMITSU PHARM CO LTD.
XX
XX Yuda K, Akiyama K, Goto T, Goto S;
XX
XX WPI; 2000-072735/06.
XX
XX Immunosuppressants with reduced side-effects, useful for preventing
PT rejection in organ and tissue transplant and as remedies for autoimmune
PT diseases and inflammatory diseases (claimed) e.g. allergy.
XX
XX
PS Example 3; Page 12; 28pp; Japanese.
XX
XX The present invention describes an immunosuppressant which contains a
CC clusterin. The present sequence represents a rat clusterin peptide from
CC an example of the present invention. Also described is a method for
CC treating rejection in organ and tissue transplant, autoimmune diseases or
CC inflammatory diseases by administering an effective dose of the
CC immunosuppressant. The immunosuppressants are useful for preventing
CC rejection in organ and tissue transplant, particularly of heart, liver,
CC lung, pancreas, kidney, small intestine, skin and bone marrow, and as
CC remedies for autoimmune diseases such as rheumatism, atopy, systemic
CC erythematous, and inflammatory diseases including allergy such as hay
CC fever. The drugs are efficacious, with little side-effects
XX
XX Sequence 14 AA;
SQ

Query Match 45.1%; Score 32; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKHYGP 9
| | | |
| | | |
Db 5 LSHYGP 10

RESULT 10
AAR88101
ID AAR88101 standard; peptide; 8 AA.
XX
XX AAR88101;
XX
XX 22-JUL-1996 (first entry)
XX
XX Bovine p32 11-cis-retinol dehydrogenase tryptic fragment P322.
XX
XX Clone p-lambda-321; bovine; p32; 11-cis-retinol; dehydrogenase;
KW 11-cis-retinaldehyde; diagnosis; retinoid; retinitis pigmentosa;
KW psoriasis; acne; cancer; T-cell leukaemia; drug development; treatment;
KW retinal pigment epithelial cell; tryptic fragment; leukemia.
XX
XX Synthetic.
XX
XX WO9534580-A1.
XX
XX 21-DEC-1995.
PD

XX
XX 06-JUN-1995; 95WO-US006256.
XX
XX 10-JUN-1994; 94US-00258418.
XX
XX 20-JAN-1995; 95US-00375962.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Hellman U, Wernstedt C, Eriksson U;
XX
XX WPI; 1996-049624/05.
XX
XX Nucleic acid encoding a retinol dehydrogenase protein - used to develop
PT prods. for the diagnosis and treatment of retinoid-linked pathological
PT conditions.
XX
XX Example 4; Page 10; 35pp; English.
XX
XX Bovine p32 11-cis-retinol dehydrogenase, which catalyses the conversion
CC of 11-cis-retinol into 11-cis-retinaldehyde, can be used for the
CC diagnosis of retinoid linked pathological conditions, e.g. retinitis
CC pigmentosa, psoriasis, acne and certain cancers (i.e. T-cell leukaemias),
CC and for the development of drugs to treat these conditions. The p32 DNA
CC clone p-lambda-321 was isolated from bovine retinal pigment epithelial
CC (RPE) cell mRNA, using degenerate primers based on the 32 kD bovine RPE
CC cell derived protein p32 tryptic fragments AAR88100-04
XX
XX Sequence 8 AA;
SQ

Query Match 43.7%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
| | | |
| | | |
Db 1 YSPGW 5

RESULT 11
AAW18339
ID AAW18339 standard; peptide; 8 AA.
XX
XX AAW18339;
XX
XX 18-AUG-1997 (first entry)
XX
XX Bovine p32 11-cis-retinol dehydrogenase tryptic peptide p322.
XX
XX 11-Cis retinol dehydrogenase; p32; 11-cis retinaldehyde;
KW retinitis pigmentosa; psoriasis; acne; cancer; diagnosis; therapy.
XX
XX Bos taurus.
XX
XX WO9719167-A1.
XX
XX 29-MAY-1997.
XX
XX 14-NOV-1996; 96WO-US018295.
XX
XX 22-NOV-1995; 95US-00562114.
XX
XX 11-OCT-1996; 96US-00729594.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Ericksson U, Simon A, Romert A;
XX
XX WPI; 1997-298106/27.
XX
XX New 11-cis retinol dehydrogenase gene - used to develop products for the
PT diagnosis and therapy of conditions such as retinitis pigmentosa,
PT psoriasis and cancers.
XX
XX Example 4; Page 11; 68pp; English.
PS

XX Tryptic peptides (AAW18338-42) were isolated from bovine retinal pigment
CC epithelial (RPE) membrane protein p32. PCR primers (see also AAT68946-49)
CC based on these primers were used to amplify cDNA (see also AAT68935)
CC coding for bovine p32 (AAW18343) from a RPE cDNA library. Peptide p322
CC corresponds to amino acids 281-288 of the p32 sequence deduced from the
CC cDNA clone. p32 is an 11-cis retinol dehydrogenase and forms a complex
CC with a component of the membrane receptor for retinol binding protein
XX
SQ Sequence 8 AA;

Query Match 43.7%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 7 YGPGW 11
DB 1 YSPGW 5

RESULT 12
AAW01990
ID AAW01990 standard; peptide; 8 AA.
XX
AC AAW01990;

DT 02-JUL-1999 (first entry)
XX
DE Tryptic peptide of bovine p32 protein.

XX p32 protein; retinol dehydrogenase; 9-cis; 11-cis; 13-cis;
KW trans retinol dehydrogenase; oligomeric protein complex;
KW membrane receptor; retinol binding protein;
KW short chain alcohol dehydrogenase family; retinaldehyde;
KW retinitis pigmentosa; skin disorder; psoriasis; acne; T-cell leukemia.
XX
OS Bos sp.

XX WO9916788-A1.

XX 08-APR-1999.

XX 21-SEP-1998; 98WO-US019836.

XX 26-SEP-1997; 97US-00937993.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Eriksson U, Simon A, Romert A;

XX WPI; 1999-255059/21.

XX New retinol dehydrogenase proteins, used to screen potential retinoid
PT drugs for treatment of various diseases, e.g. retinitis pigmentosa.
XX

XX Example 4; Page 14; 8pp; English.

XX AAW01989-93 represent peptide obtained after tryptic digest of a p32
CC protein, isolated in the course of the invention. The specification
CC describes proteins having retinol dehydrogenase activity, such as 9-cis,
CC 11-cis, 13-cis, or trans retinol dehydrogenase activity. These proteins
CC form oligomeric protein complexes with the components of the membrane
CC receptor for retinol binding protein. The retinol dehydrogenase proteins
CC are members of the short chain alcohol dehydrogenase family. The
CC recombinant enzymes can be used to produce 9-cis and 11-cis
CC retinaldehydes. The proteins and nucleic acids encoding them can be used
CC to screen potential retinoid drugs for treatment of various diseases,
CC e.g. diseases of the eye such as retinitis pigmentosa and skin disorders
CC such as psoriasis and acne. Certain T-cell leukemias may also be tested
CC by retinoid drugs. Antibodies against the protein can be used to monitor
CC pathological conditions characterized by aberrant levels of a receptor
CC for retinol binding protein
XX

SQ Sequence 8 AA;
Query Match 43.7%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 7 YGPGW 11
DB 1 YSPGW 5

RESULT 13
AAR31264
ID AAR31264 standard; peptide; 9 AA.
XX
AC AAR31264;

DT 12-FEB-1993 (first entry)
XX

DE HIV principal determinant peptide.

XX AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
KW meningitidis b; outer membrane protein complex; OMPC; CPND23.
XX
OS Synthetic.

XX Key Location/Qualifiers
FH Modified-site 1 /label= Nle
FT /note= "this position is linked to the OMPC of the
FT conjugate"

FT Modified-site 2 /note= "epsilon-amino group is condensed with C-terminal
FT COOH to form cyclic peptide"

FT Modified-site 9 /note= "forms amide bond with epsilon-amino of Lys(2) to
FT give cyclic molecule"

XX EP467700-A.

XX 22-JAN-1992.

XX 19-JUL-1991; 91EP-00306598.

XX 19-JUL-1990; 90US-00555339.

XX 19-JUL-1990; 90US-00555966.

XX 19-JUN-1991; 91US-00715276.

XX 19-JUN-1991; 91US-00715278.

XX (MERI) MERCK & CO INC.

XX Leanza WJ, Marburg S, Tolman RL, Emini EA;

XX WPI; 1992-026505/04.

XX Conjugate proteins comprising HIV peptide components - useful for
PT preparing vaccines for e.g. AIDS or for treating infections.
XX

XX Claim 12; Page 54; 63pp; English.

XX The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the
CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMPC) of Neisseria
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND23) is an example of a

CC antibodies can be used for passively protecting against infection by HIV,
CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays
XX
SQ Sequence 9 AA;

Query Match 43.7%; Score 31; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10
|||
Db 2 KHIGPG 7

RESULT 16

AAW03401
ID AAW03401 standard; peptide; 9 AA.

AC AAW03401;

DT 07-OCT-1996 (first entry)

DE HIV principal neutralizing determinant CPND815.

KW conjugate; PND; HIV; principal neutralizing determinant; OMPC;
KW outer membrane protein complex; anionic spacer; vaccine;
KM human immunodeficiency virus; water-soluble.

OS Synthetic.

Key Location/Qualifiers
Modified-site 1

/label= N1e
/note= "the N-terminal of this norleucine residue is
linked to Neisseria meningitidis OMPC via a specified
anionic spacer group"

Modified-site 2

/label= cycle
/note= "the epsilon-amino of this residue forms a peptide
bond with the terminal carboxy group of Ala(9), giving a
cyclic peptide"

Modified-site 9

/note= "the carboxy group is condensed onto the epsilon-
amino of Lys(2). See above"

GB2271995-A.

04-MAY-1994.

12-OCT-1993; 93GB-00020943.

15-OCT-1992; 92US-00963327.

(MERI) MERCK & CO INC.

Tolman RL, Marburg S, Leanza WL, Lombardo VK;

WPI; 1994-128412/16.

New conjugates of outer membrane protein and HIV epitope - for generating
HIV-neutralizing response, have components joined by anionic spacer to
ensure solubility of prod.

Claim 6; Page 68; 73pp; English.

A new conjugate immunogen comprises (a) the OMPC of Neisseria
meningitidis b as a protein carrier, (b) a principal neutralizing
determinant (PND) of HIV as a peptidyl epitope against which immune
responses are desired, and (c) a low mol. wt. anionic spacer linking (a)
and (b). The conjugate is water-soluble, yet can carry a high peptide
epitope loading. It is useful as a vaccine against HIV. The present
sequence is an example of a PND used in the conjugate

XX
SQ Sequence 9 AA;

Query Match 43.7%; Score 31; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10
|||
Db 2 KHIGPG 7

RESULT 17

AAR31271

ID AAR31271 standard; peptide; 10 AA.

AC AAR31271;

DT 12-FEB-1993 (first entry)

DE HIV principal determinant peptide.

KW AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
KW meningitidis b; outer membrane protein complex; OMPC; CPND30.

OS Synthetic.

Key Location/Qualifiers
Modified-site 1

/label= N1e
/note= "this position is linked to the OMPC of the
conjugate"

Modified-site 2

/note= "epsilon-amino group is condensed with C-terminal
COOH to form cyclic peptide"

Modified-site 10

/note= "forms amide bond with epsilon-amino of Lys(2) to
give cyclic molecule"

EP467700-A.

22-JAN-1992.

19-JUL-1991; 91EP-00306598.

19-JUL-1990; 90US-00555339.

19-JUL-1990; 90US-00555966.

19-JUN-1991; 91US-00715276.

19-JUN-1991; 91US-00715278.

(MERI) MERCK & CO INC.

Leanza WJ, Marburg S, Tolman RL, Emini EA;

WPI; 1992-026505/04.

Conjugate proteins comprising HIV peptide components - useful for
preparing vaccines for e.g. AIDS or for treating infections.

Claim 12; Page 55; 63pp; English.

The invention relates to a co-conjugate comprising an immunogenic protein
or protein complex having a first set of covalent linkages to low
molecular weight moieties which have an anionic or polyanionic character
at physiological pH, and a second set of covalent linkages to peptides
comprising HIV principal neutralizing determinants (PND's) or
immunologically equivalent peptides. Preferably at least one set of the
covalent linkages is comprised of maleimide derivatives; the
(poly)anionic moiety is composed of one to five residues of the anionic
form of a carboxylic, sulphonate or phosphonic acid; the immunogenic
protein is the outer membrane protein complex (OMPC) of Neisseria
meningitidis b; and the PND peptide has a linear structure, a disulphide-
bonded cyclic structure, an amide-bonded cyclic structure or a thioether-

CC bonded cyclic structure. The present sequence (CPND30) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10
Db 2 KHIGPG 7

RESULT 18
AAR31260
ID AAR31260 standard; peptide; 10 AA.

AC AAR31260;

DT 12-FEB-1993 (first entry)

DE HIV principal determinant peptide.

KW AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
meningitidis b; outer membrane protein complex; OMPC; CPND14.

OS Synthetic.

Key Location/Qualifiers
Modified-site 1
/label= Nle
/note= "this position is linked to the OMPC of the
conjugate"

Modified-site 2
/note= "D-Lys; and epsilon-amino group is condensed with
C-terminal COOH to form cyclic peptide"
Modified-site 10
/note= "forms amide bond with epsilon-amino of Lys(2) to
give cyclic molecule"

EP467700-A.

22-JAN-1992.

19-JUL-1991; 91EP-00306598.

19-JUL-1990; 90US-00555339.

19-JUL-1990; 90US-00555966.

19-JUN-1991; 91US-00715276.

19-JUN-1991; 91US-00715278.

(MERI) MERCK & CO INC.
Leanza WJ, Marburg S, Tolman RL, Emini EA;
WPI; 1992-026505/04.

Conjugate proteins comprising HIV peptide components - useful for
preparing vaccines for e.g. AIDS or for treating infections.

Claim 12; Page 54; 63pp; English.

The invention relates to a co-conjugate comprising an immunogenic protein
or protein complex having a first set of covalent linkages to low
molecular weight moieties which have an anionic or polyanionic character
at physiological pH, and a second set of covalent linkages to peptides
comprising HIV principal neutralizing determinants (PND's) or
immunologically equivalent peptides. Preferably at least one set of the

CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMPC) of Neisseria
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND14) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10
Db 2 KHIGPG 7

RESULT 19
AAR31268
ID AAR31268 standard; peptide; 10 AA.

AC AAR31268;

DT 12-FEB-1993 (first entry)

DE HIV principal determinant peptide.

KW AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
meningitidis b; outer membrane protein complex; OMPC; CPND27.

OS Synthetic.

Key Location/Qualifiers
Modified-site 1
/label= Nle
/note= "this position is linked to the OMPC of the
conjugate"
Modified-site 2
/note= "epsilon-amino group is condensed with C-terminal
COOH to form cyclic peptide"
Modified-site 10
/note= "D-Phe; and forms amide bond with epsilon-amino of
Lys(2) to give cyclic molecule"

EP467700-A.

22-JAN-1992.

19-JUL-1991; 91EP-00306598.

19-JUL-1990; 90US-00555339.

19-JUL-1990; 90US-00555966.

19-JUN-1991; 91US-00715276.

19-JUN-1991; 91US-00715278.

(MERI) MERCK & CO INC.
Leanza WJ, Marburg S, Tolman RL, Emini EA;
WPI; 1992-026505/04.

Conjugate proteins comprising HIV peptide components - useful for
preparing vaccines for e.g. AIDS or for treating infections.

Claim 12; Page 55; 63pp; English.

XX

CC The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the
CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMPC) of *Neisseria*
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND27) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
Db 2 KHIGPG 7

RESULT 20
ID AAR31272 standard; peptide; 10 AA.
XX
AC AAR31272;
XX
DT 12-FEB-1993 (first entry)
XX
DE HIV principal determinant peptide.
XX
KW AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; *Neisseria*;
KW meningitidis b; outer membrane protein complex; OMPC; CPND31.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N(epsilon)-substituted by Nle, which in turn is
FT bonded to the OMPC of the conjugate; and N(alpha)-
FT condensed by side-chain COOH of Glu(10) to form a cyclic
FT molecule"
FT Modified-site 10
FT /note= "Glu-NH2; and omega-COOH condenses with the alpha-
FT amino group of Lys(1), giving cyclic peptide"
XX
PN EPA67700-A.
XX
PD 22-JAN-1992.
XX
PF 19-JUL-1991; 91BP-00306598.
XX
PR 19-JUL-1990; 90US-00555339.
PR 19-JUL-1990; 90US-00555966.
PR 19-JUN-1991; 91US-00715276.
PR 19-JUN-1991; 91US-00715278.
XX
PA (MERI) MERCK & CO INC.
XX
PI Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX
DR WPI; 1992-026505/04.
XX
PT Conjugate proteins comprising HIV peptide components - useful for

PT preparing vaccines for e.g. AIDS or for treating infections.
XX
PS Claim 12; Page 55; 63pp; English.
XX
CC The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the
CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMPC) of *Neisseria*
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND31) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
Db 1 KHIGPG 6

RESULT 21
ID AAR31256 standard; peptide; 10 AA.
XX
AC AAR31256;
XX
DT 12-FEB-1993 (first entry)
XX
DE HIV principal determinant peptide.
XX
KW AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; *Neisseria*;
KW meningitidis b; outer membrane protein complex; OMPC; CPND8.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= Nle
FT /note= "this position is linked to the OMPC of the
FT conjugate"
FT Modified-site 2
FT /note= "epsilon-amino group is condensed with C-terminal
FT COOH to form cyclic peptide"
FT Modified-site 10
FT /note= "forms amide bond with epsilon-amino of Lys(2) to
FT give cyclic molecule"
XX
PN EPA67700-A.
XX
PD 22-JAN-1992.
XX
PF 19-JUL-1991; 91BP-00306598.
XX
PR 19-JUL-1990; 90US-00555339.
PR 19-JUL-1990; 90US-00555966.
PR 19-JUN-1991; 91US-00715276.
PR 19-JUN-1991; 91US-00715278.
XX
PA (MERI) MERCK & CO INC.

XX Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX WPI; 1992-026505/04.
DR
XX Conjugate proteins comprising HIV peptide components - useful for
PT preparing vaccines for e.g. AIDS or for treating infections.
PT
XX
PS Claim 12; Page 53; 63pp; English.
XX
CC The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the
CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMP) of *Neisseria*
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND8) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
|||
Db 2 KHIGPG 7

RESULT 22
AAR30018
ID AAR30018 standard; peptide; 10 AA.
XX
AC AAR30018;
XX
DT 25-MAR-2003 (revised)
DT 28-APR-1993 (first entry)
XX
DE HIV CPND31.
XX
KW Human immunodeficiency virus; AIDS; PND; MIEP; conjugate;
KW major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen;
KW passive immunisation; principle neutralising determinant.
XX
OS Human immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= Nle
FT Modified-site 2.10 /note= "Lys-NH-NH-CO(CH2)2-CH(CONH2)-NH-CO-Phe"
FT
XX
PN EP519554-A1.
XX
PD 23-DEC-1992.
XX
PF 11-JUN-1992; 92EP-00201693.
XX
PR 19-JUN-1991; 91US-00715273.
XX
PA (MERI) MERCK & CO INC.
XX

PI Emini A, Liu MA, Marburg S, Tolman RL;
XX WPI; 1992-425771/52.
DR
XX Conjugates of HIV-1 PND peptide(s) with the MIEP of *Neisseria*
PT meningitidis - useful as a vaccine for treating and preventing HIV-1
PT infection, e.g. AIDS in humans.
PT
XX
PS Claim 9; Page 60; 66pp; English.
XX
CC The peptide is HIV principle neutralising determinant CPND31 and is used
CC as part of a conjugate comprising the major immune enhancing protein
CC (MIEP) of *Neisseria meningitidis* covalently linked to the HIV PND. The
CC conjugate may be used to prepare vaccines against HIV infections, e.g.
CC AIDS, as research tools for studying PND structure- function
CC relationships, or as immunogens for use in the passive immunisation of
CC humans. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
|||
Db 2 KHIGPG 7

RESULT 23
AAR31309
ID AAR31309 standard; peptide; 10 AA.
XX
AC AAR31309;
XX
DT 11-FEB-1993 (first entry)
XX
DE Cyclic HIV principal neutralizing determinant peptide.
XX
KW Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;
KW immunogen; ELISA; analysis; CPND31.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N(epsilon)-acylated by H-Nle; N(alpha) condensed
FT with side-chain COOH of C-terminal Glu to form cyclic
FT molecule"
FT Modified-site 10 /note= "Glu-NH2; omega-COOH forms cyclic amide bond with
FT alpha-NH2 of Lys(1)"
FT
XX
PN EP471453-A.
XX
PD 19-FEB-1992.
XX
PF 19-JUL-1991; 91EP-00306582.
XX
PR 19-JUL-1990; 90US-00555112.
XX
PA (MERI) MERCK & CO INC.
XX
PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;
XX WPI; 1992-058511/08.
XX
PF New cyclic HIV principal neutralising determinant peptide(s) - used as
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.
XX
PS Claim 4; Page 22; 25pp; English.
XX
CC The peptide (CPND31) is a specifically claimed example of HIV principal

CC neutralizing determinant peptides which are covered generically in Claims
CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result
CC of a lactam bridge between an NH₂ on the N-terminal side of the loop
CC amino acids and a COOH on the C-terminal side of the loop amino acids.
CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND
CC peptides (CPND's) may be used as analytical tools and as reagents in
CC ELISA assays. They may also be conjugated to an immunogenic carrier (a
CC protein and/or a polysaccharide; e.g. PRP or OMPC) to give a product
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing
CC immune responses and for formulating vaccines to prevent HIV disease,
CC including AIDS and ARC, or for treating humans afflicted with HIV disease
CC such as AIDS or ARC

XX Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10
|||
Db 1 KHIGPG 6

RESULT 24

AAR31293
ID AAR31293 standard; peptide; 10 AA.

XX AAR31293;

DT 11-FEB-1993 (first entry)

XX Cyclic HIV principal neutralizing determinant peptide.

DE Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;

KW immunogen; ELISA; analysis; CPND7; CPND8.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "Z-Nle (giving CPND7) or H-Nle (giving CPND8)"

FT Modified-site 2

FT /note= "forms cyclic lactam bond, via epsilon-NH₂, with C

FT -terminal COOH"

FT Modified-site 10

FT /note= "forms cyclic amide bond with epsilon-NH₂ of

FT Lys(2)"

XX EP471453-A.

XX 19-FEB-1992.

XX 19-JUL-1991; 91EP-00306582.

XX 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

XX Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

XX WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 20; 25pp; English.

XX The peptides (CPND7 and CPND8) are specifically claimed examples of HIV

CC principal neutralizing determinant peptides which are covered generically

CC in Claims 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as

CC a result of a lactam bridge between an NH₂ on the N-terminal side of the

CC loop amino acids and a COOH on the C-terminal side of the loop amino
CC acids. The bond is less labile than a disulphide bond. The stable cyclic
CC HIV PND peptides (CPND's) may be used as analytical tools and as reagents
CC in ELISA assays. They may also be conjugated to an immunogenic carrier (a
CC protein and/or a polysaccharide; e.g. PRP or OMPC) to give a product
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing
CC immune responses and for formulating vaccines to prevent HIV disease,
CC including AIDS and ARC, or for treating humans afflicted with HIV disease
CC such as AIDS or ARC

XX Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10
|||
Db 2 KHIGPG 7

RESULT 25

AAR31308
ID AAR31308 standard; peptide; 10 AA.

XX AAR31308;

DT 11-FEB-1993 (first entry)

XX Cyclic HIV principal neutralizing determinant peptide.

DE Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;

KW immunogen; ELISA; analysis; CPND30.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "Z-Nle"

FT Modified-site 2

FT /note= "forms cyclic lactam bond, via epsilon-NH₂, with C

FT -terminal COOH"

FT Modified-site 10

FT /note= "forms cyclic amide bond with epsilon-NH₂ of

FT Lys(2)"

XX EP471453-A.

XX 19-FEB-1992.

XX 19-JUL-1991; 91EP-00306582.

XX 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

XX Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

XX WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 22; 25pp; English.

XX The peptide (CPND30) is a specifically claimed example of HIV principal

CC neutralizing determinant peptides which are covered generically in Claims

CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result

CC of a lactam bridge between an NH₂ on the N-terminal side of the loop

CC amino acids and a COOH on the C-terminal side of the loop amino acids.

CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND

CC peptides (CPND's) may be used as analytical tools and as reagents in

CC ELISA assays. They may also be conjugated to an immunogenic carrier (a
 CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product
 CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing
 CC immune responses and for formulating vaccines to prevent HIV disease,
 CC including AIDS or ARC, or for treating humans afflicted with HIV disease
 CC such as AIDS or ARC

XX
 SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
 |||||
 Db 2 KHIGPG 7

RESULT 26

AAR31297
 ID AAR31297 standard; peptide; 10 AA.

XX AAR31297;

DT 11-FEB-1993 (first entry)

XX Cyclic HIV principal neutralizing determinant peptide.

DE Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;
 KW immunogen; ELISA; analysis; CPND14.

XX Synthetic.

OS
 FH Key Location/Qualifiers

FT Modified-site 1 /label= N1e

FT Modified-site 2 /note= "2-N1e"

FT Modified-site 2 /note= "D-Lys; and forms cyclic lactam bond, via epsilon-NH2, with C-terminal COOH"

FT Modified-site 10 /note= "forms cyclic amide bond with epsilon-NH2 of Lys(2)"

XX EP471453-A.

XX 19-FEB-1992.

XX 19-JUL-1991; 91EP-00306582.

XX 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

XX WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as
 PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 20; 25pp; English.

CC The peptide (CPND14) is a specifically claimed example of HIV principal
 CC neutralizing determinant peptides which are covered generically in Claims
 CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result
 CC of a lactam bridge between an NH2 on the N-terminal side of the loop
 CC amino acids and a COOH on the C-terminal side of the loop amino acids.
 CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND
 CC peptides (CPND's) may be used as analytical tools and as reagents in
 CC ELISA assays. They may also be conjugated to an immunogenic carrier (a
 CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product
 CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing

CC immune responses and for formulating vaccines to prevent HIV disease,
 CC including AIDS and ARC, or for treating humans afflicted with HIV disease
 CC such as AIDS or ARC

XX
 SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
 |||||
 Db 2 KHIGPG 7

RESULT 27

AAR31305
 ID AAR31305 standard; peptide; 10 AA.

XX AAR31305;

DT 11-FEB-1993 (first entry)

XX Cyclic HIV principal neutralizing determinant peptide.

DE Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;
 KW immunogen; ELISA; analysis; CPND27.

XX Synthetic.

OS
 FH Key Location/Qualifiers

FT Modified-site 1 /label= N1e

FT Modified-site 2 /note= "forms cyclic lactam bond, via epsilon-NH2, with C-terminal COOH"

FT Modified-site 10 /note= "D-Phe; and forms cyclic amide bond with epsilon-NH2 of Lys(2)"

XX EP471453-A.

XX 19-FEB-1992.

XX 19-JUL-1991; 91EP-00306582.

XX 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

XX WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as
 PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 22; 25pp; English.

CC The peptide (CPND27) is a specifically claimed example of HIV principal
 CC neutralizing determinant peptides which are covered generically in Claims
 CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result
 CC of a lactam bridge between an NH2 on the N-terminal side of the loop
 CC amino acids and a COOH on the C-terminal side of the loop amino acids.
 CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND
 CC peptides (CPND's) may be used as analytical tools and as reagents in
 CC ELISA assays. They may also be conjugated to an immunogenic carrier (a
 CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product
 CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing
 CC immune responses and for formulating vaccines to prevent HIV disease,
 CC including AIDS and ARC, or for treating humans afflicted with HIV disease
 CC such as AIDS or ARC

SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10

Db 2 KHIGPG 7

RESULT 28

AAR26696
ID AAR26696 standard; peptide; 10 AA.

XX AAR26696;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

KW Human immunodeficiency virus; principal neutralizing determinant;

KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND14.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "bonded via N-terminal to polysaccharide- protein complex"

FT Modified-site 2

FT /note= "D-Lys; epsilon-amino forms cyclic peptide with C-terminal COOH group"

FT Modified-site 10

FT /note= "condenses with side chain NH2 of Lys(2) to give cyclic peptide"

PN EP468714-A.

PD 29-JAN-1992.

PF 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555974.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

PA (MERI) MERCK & CO INC.

PI Marburg S, Tolman RL, Emini EA;

DR WPI; 1992-034437/05.

PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to produce antibodies to prevent or treat HIV infection.

PS Claim 9; Page 54; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing determinant (PND), or an immunologically equivalent peptide (PEP), covalently coupled to an immunogenic protein or protein complex through an anionic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMPC) of Neisseria meningitidis b and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. CC The present sequence (CPND14) is an example of a PND peptide component. CC The conjugates are used for inducing HIV-neutralising antibodies or for making vaccines to prevent for contracting HIV infection or disease. The CC antibodies can be used for passively protecting against infection by HIV, or for protecting against proliferation of HIV post-infection, or for CC treating AIDS, or in diagnostic assays

XX SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10

Db 2 KHIGPG 7

RESULT 29

AAR26691
ID AAR26691 standard; peptide; 10 AA.

XX AAR26691;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

KW Human immunodeficiency virus; principal neutralizing determinant;

KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND8.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "bonded via N-terminal to polysaccharide- protein complex"

FT Modified-site 2

FT /note= "epsilon-amino forms cyclic peptide with C-terminal COOH group"

FT Modified-site 10

FT /note= "condenses with side chain NH2 of Lys(2) to give cyclic peptide"

PN EP468714-A.

PD 29-JAN-1992.

PF 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555974.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

PA (MERI) MERCK & CO INC.

PI Marburg S, Tolman RL, Emini EA;

DR WPI; 1992-034437/05.

PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to produce antibodies to prevent or treat HIV infection.

PS Claim 9; Page 54; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing determinant (PND), or an immunologically equivalent peptide (PEP), covalently coupled to an immunogenic protein or protein complex through an anionic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMPC) of Neisseria meningitidis b and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. CC The present sequence (CPND8) is an example of a PND peptide component. CC The conjugates are used for inducing HIV-neutralising antibodies or for making vaccines to prevent for contracting HIV infection or disease. The CC antibodies can be used for passively protecting against infection by HIV, or for protecting against proliferation of HIV post-infection, or for CC

CC treating AIDS, or in diagnostic assays
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHGPG 10
|||
2 KHIGPG 7

Db

RESULT 30
AAR26707
ID AAR26707 standard; peptide; 10 AA.

XX AAR26707;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;
KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND30.
XX
OS Synthetic.

XX Key
FH Modified-site 1 Location/Qualifiers
FT /label= Nle

FT /note= "bonded via N-terminal to polysaccharide- protein
FT complex"

FT Modified-site 2 /note= "epsilon-amino forms cyclic peptide with C-

FT terminal COOH group"

FT Modified-site 10 /note= "condenses with side chain NH2 of Lys(2) to give
FT cyclic peptide"

XX EP468714-A.

XX 29-JAN-1992.

PF 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555974.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

XX (MERI) MERCK & CO INC.

XX Marburg S, Tolman RL, Emini EA;

XX WPI; 1992-034437/05.

DR HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

PT produce antibodies to prevent or treat HIV infection.

XX Claim 9; Page 56; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing
CC determinant (PND), or an immunologically equivalent peptide (PEP),
CC covalently coupled to an immunogenic protein or protein complex through
CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
CC The present sequence (CPND30) is an example of a PND peptide component.
CC The conjugates are used for inducing HIV-neutralising antibodies or for
CC making vaccines to prevent contraction of HIV infection or disease. The
CC antibodies can be used for passively protecting against infection by HIV,

CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays
XX

SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHGPG 10
|||
2 KHIGPG 7

Db

RESULT 31
AAR26708
ID AAR26708 standard; peptide; 10 AA.

XX AAR26708;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;
KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND31.
XX
OS Synthetic.

XX Key
FH Modified-site 1 Location/Qualifiers
FT /note= "N(epsilon)-condensed by Nle, where the N-terminal

FT of the Nle bonds to polysaccharide- protein complex;
FT N(alpha)-condensed by omega-COOH of Glu(10) to give

FT Modified-site 10 /note= "Glu-NH2; where omega-COOH condenses onto alpha-

FT cyclic peptide" NH2 of Lys(1) to form cyclic peptide"

XX EP468714-A.

XX 29-JAN-1992.

PF 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555974.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

XX (MERI) MERCK & CO INC.

XX Marburg S, Tolman RL, Emini EA;

XX WPI; 1992-034437/05.

DR HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

PT produce antibodies to prevent or treat HIV infection.

XX Claim 9; Page 56; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing
CC determinant (PND), or an immunologically equivalent peptide (PEP),
CC covalently coupled to an immunogenic protein or protein complex through
CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
CC The present sequence (CPND31) is an example of a PND peptide component.
CC The conjugates are used for inducing HIV-neutralising antibodies or for
CC making vaccines to prevent contraction of HIV infection or disease. The
CC antibodies can be used for passively protecting against infection by HIV,
CC or for protecting against proliferation of HIV post-infection, or for

CC treating AIDS, or in diagnostic assays
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
| | | | |
Db 1 KHIGPG 6

RESULT 32

AAR26704

ID AAR26704 standard; peptide; 10 AA.

XX AAR26704;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;

KW outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; CPND27.

XX Synthetic.

OS Key Location/Qualifiers

FH Modified-site 1

FT /label= Nle

FT /note= "Bonded via N-terminal to polysaccharide- protein complex"

FT Modified-site 2

FT /note= "epsilon-amino forms cyclic peptide with C-terminal COOH group"

FT Modified-site 10

FT /note= "D-Phe; condenses with side chain NH2 of Lys(2) to give cyclic peptide"

XX EP468714-A.

PD 29-JAN-1992.

PF 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555558.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

PA (MERI) MERCK & CO INC.

PI Marburg S, Tolman RL, Emini EA;

DR WPI; 1992-034437/05.

PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to produce antibodies to prevent or treat HIV infection.

PS Claim 9; Page 55; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing determinant (PND), or an immunologically equivalent peptide (PEP), covalently coupled to an immunogenic protein or protein complex through an anionic polysaccharide linker. Pref. the immunogenic protein is the outer membrane protein complex (OMPC) of Neisseria meningitidis b and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. The present sequence (CPND27) is an example of a PND peptide component. CC The conjugates are used for inducing HIV-neutralising antibodies or for making vaccines to prevent contraction of HIV infection or disease. The CC antibodies can be used for passively protecting against infection by HIV,

CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays
XX
SQ Sequence 10 AA;

Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
| | | | |
Db 2 KHIGPG 7

RESULT 33

AAW03407

ID AAW03407 standard; peptide; 10 AA.

XX AAW03407;

DT 10-OCT-1996 (first entry)

DE HIV principal neutralizing determinant CPND8.

XX conjugate; PND; HIV; principal neutralizing determinant; OMPC;

KW outer membrane protein complex; anionic spacer; vaccine;

XX human immunodeficiency virus; water-soluble.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "the N-terminal of this norleucine residue can be linked to Neisseria meningitidis OMPC via a specified anionic spacer group"

FT Modified-site 2

FT /label= cycle

FT /note= "the epsilon-amino of this residue forms a peptide bond with the terminal carboxy group of Phe(10), giving a cyclic peptide"

FT Modified-site 10

FT /note= "the carboxy group is condensed onto the epsilon-amino of Lys(2). See above"

XX GB2271995-A.

PD 04-MAY-1994.

PF 12-OCT-1993; 93GB-00020943.

PR 15-OCT-1992; 92US-00963327.

PA (MERI) MERCK & CO INC.

PI Tolman RL, Marburg S, Leanza WL, Lombardo VK;

DR WPI; 1994-128412/16.

PT New conjugates of outer membrane protein and HIV epitope - for generating HIV-neutralising response, have components joined by anionic spacer to ensure solubility of prod.

PS Example 25; Page 42; 73pp; English.

XX A new conjugate immunogen comprises (a) the OMPC of Neisseria meningitidis b as a protein carrier, (b) a principal neutralizing determinant (PND) of HIV as a peptidyl epitope against which immune responses are desired, and (c) a low mol. wt. anionic spacer linking (a) and (b). The conjugate is water-soluble, yet can carry a high peptide epitope loading. It is useful as a vaccine against HIV. The present CC sequence is an example of a PND which can be used in the conjugate

Sequence 10 AA;
Query Match 43.7%; Score 31; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 KHYGPG 10
Db 2 KHIGPG 7
RESULT 34
AAR31270
ID AAR31270 standard; peptide; 11 AA.
AC AAR31270;
XX 12-FEB-1993 (first entry)
DT HIV principal determinant peptide.
DE
XX
XX AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
KW meningitidis b; outer membrane protein complex; OMPC; CPND29.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= Nle
FT /note= "this position is linked to the OMPC of the
FT conjugate"
FT Modified-site 2
FT /note= "epsilon-amino group is condensed with C-terminal
FT COOH to form cyclic peptide"
FT Modified-site 11
FT /note= "D-Val; and forms amide bond with epsilon-amino of
FT Lys(2) to give cyclic molecule"
XX
XX EP467700-A.
PN 22-JAN-1992.
PD
XX 19-JUL-1991; 91EP-00306598.
PF
XX 19-JUL-1990; 90US-00555339.
PR 19-JUL-1990; 90US-00555966.
PR 19-JUN-1991; 91US-00715276.
PR 19-JUN-1991; 91US-00715278.
XX
PA (MERI) MERCK & CO INC.
XX
PI Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX WPI; 1992-026505/04.
DR
XX
PT Conjugate proteins comprising HIV peptide components - useful for
PT preparing vaccines for e.g. AIDS or for treating infections.
XX
XX Claim 12; Page 55; 63pp; English.
PS
XX
XX The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the
CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMPC) of Neisseria
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND29) is an example of a

PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
XX Sequence 11 AA;
QY 5 KHYGPG 10
Db 2 KHIGPG 7
RESULT 35
AAR31257
ID AAR31257 standard; peptide; 11 AA.
XX
XX AAR31257;
AC
XX 12-FEB-1993 (first entry)
DT
XX
DE HIV principal determinant peptide.
XX
XX AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
KW meningitidis b; outer membrane protein complex; OMPC; CPND9.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= Ac-Cys
FT /note= "bonds via this site to the OMPC of the conjugate"
FT Modified-site 2
FT /label= Nle
FT Modified-site 3
FT /note= "epsilon-amino group is condensed with C-terminal
FT COOH to form cyclic peptide"
FT Modified-site 11
FT /note= "forms amide bond with epsilon-amino of Lys(3) to
FT give cyclic molecule"
XX
XX EP467700-A.
PN 22-JAN-1992.
PD
XX 19-JUL-1991; 91EP-00306598.
PF
XX 19-JUL-1990; 90US-00555339.
PR 19-JUL-1990; 90US-00555966.
PR 19-JUN-1991; 91US-00715276.
PR 19-JUN-1991; 91US-00715278.
XX
PA (MERI) MERCK & CO INC.
XX
PI Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX WPI; 1992-026505/04.
DR
XX
PT Conjugate proteins comprising HIV peptide components - useful for
PT preparing vaccines for e.g. AIDS or for treating infections.
XX
XX Claim 12; Page 53; 63pp; English.
PS
XX
XX The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the

CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMP) of *Neisseria*
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (CPND9) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease

SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHVGPG 10
Db 3 KHIGPG 8

RESULT 36

ID AAR31307 standard; peptide; 11 AA.

XX AAR31307;

DT 11-FEB-1993 (first entry)

XX Cyclic HIV principal neutralizing determinant peptide.

XX Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;
XX immunogen; ELISA; analysis; CPND29.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "2-Nle"

FT Modified-site 2

FT /note= "forms cyclic lactam bond, via epsilon-NH2, with C

FT Modified-site 11

FT /note= "D-Val; and forms cyclic amide bond with epsilon

FT NH2 of Lys(2)"

PN EP471453-A.

PD 19-FEB-1992.

PF 19-JUL-1991; 91EP-00306582.

PR 19-JUL-1990; 90US-00555112.

PA (MERI) MERCK & CO INC.

PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

DR WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

PS Claim 4; Page 22; 25pp; English.

XX The peptide (CPND29) is a specifically claimed example of HIV principal
CC neutralizing determinant peptides which are covered generically in Claims
CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result
CC of a lactam bridge between an NH2 on the N-terminal side of the loop

CC amino acids and a COOH on the C-terminal side of the loop amino acids.
CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND
CC peptides (CPND's) may be used as analytical tools and as reagents in
CC ELISA assays. They may also be conjugated to an immunogenic carrier (a
CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing
CC immune responses and for formulating vaccines to prevent HIV disease,
CC including AIDS and ARC, or for treating humans afflicted with HIV disease
CC such as AIDS or ARC

SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHVGPG 10
Db 2 KHIGPG 7

RESULT 37

ID AAR31294 standard; peptide; 11 AA.

XX AAR31294;

DT 11-FEB-1993 (first entry)

XX Cyclic HIV principal neutralizing determinant peptide.

XX Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; ARC; vaccine;
XX immunogen; ELISA; analysis; CPND9; CPND10.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Ac-Cys (Acm) (giving CPND10) or Ac-Cys (giving

FT CPND9)"

FT Modified-site 2

FT /label= Nle

FT /note= "forms cyclic lactam bond, via epsilon-NH2, with C

FT Modified-site 11

FT /note= "forms cyclic amide bond with epsilon-NH2 of

FT Lys(3)"

PN EP471453-A.

PD 19-FEB-1992.

PF 19-JUL-1991; 91EP-00306582.

PR 19-JUL-1990; 90US-00555112.

PA (MERI) MERCK & CO INC.

PI Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

DR WPI; 1992-058511/08.

PT New cyclic HIV principal neutralising determinant peptide(s) - used as
PT laboratory tools and as vaccines against HIV, AIDS, arc etc.

PS Claim 4; Page 20; 25pp; English.

XX The peptides (CPND9 and CPND10) are specifically claimed examples of HIV
CC principal neutralizing determinant peptides which are covered generically
CC in Claims 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as
CC a result of a lactam bridge between an NH2 on the N-terminal side of the
CC loop amino acids and a COOH on the C-terminal side of the loop amino

CC acids. The bond is less labile than a disulphide bond. The stable cyclic
CC HIV PND peptides (cPND's) may be used as analytical tools and as reagents
CC in ELISA assays. They may also be conjugated to an immunogenic carrier (a
CC protein and/or a polysaccharide; e.g. PRP or OMPC) to give a product
CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing
CC immune responses and for formulating vaccines to prevent HIV disease,
CC including AIDS and ARC, or for treating humans afflicted with HIV disease
CC such as AIDS or ARC
XX
SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
|||
Db 3 KHIGPG 8

RESULT 38

AAR26692
ID AAR26692 standard; peptide; 11 AA.

XX AAR26692;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

XX
KW Human immunodeficiency virus; principal neutralizing determinant;
KM outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; cPND9.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Modified-site 1 /note= "Ac-Cys, bonded to polysaccharide- protein

FT Modified-site 2 complex"

FT Modified-site 3 /label= Nle

FT Modified-site /note= "epsilon-amino forms cyclic peptide with C-

FT Modified-site 11 /note= "condenses with side chain NH2 of Lys(3) to give

FT Modified-site cyclic peptide"

XX
PN EP468714-A.

XX
PD 29-JAN-1992.

XX
PF 19-JUL-1990; 90US-00555558.

XX
PR 19-JUL-1990; 90US-00555558.

XX
PR 19-JUL-1990; 90US-00555974.

XX
PR 19-JUN-1991; 91US-00715275.

XX
PR 19-JUN-1991; 91US-00715277.

XX
PA (MERI) MERCK & CO INC.

XX
PI Marburg S, Tolman RL, Emini EA;

XX
XX WPI; 1992-034437/05.

XX
PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

XX
PT produce antibodies to prevent or treat HIV infection.

XX
PS Claim 9; Page 54; 63pp; English.
XX
CC The invention relates to a conjugate of an HIV principal neutralizing
CC determinant (PND), or an immunologically equivalent peptide (PEP),
CC covalently coupled to an immunogenic protein or protein complex through

CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
CC The present sequence (cPND9) is an example of a PND peptide component.
CC The conjugates are used for inducing HIV-neutralising antibodies or for
CC making vaccines to prevent contraction of HIV infection or disease. The
CC antibodies can be used for passively protecting against infection by HIV,
CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays
XX
SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGPG 10
|||
Db 3 KHIGPG 8

RESULT 39

AAR26706
ID AAR26706 standard; peptide; 11 AA.

XX AAR26706;

DT 09-FEB-1993 (first entry)

DE HIV-PND-polysaccharide-protein conjugate vaccine.

XX
KW Human immunodeficiency virus; principal neutralizing determinant;
KM outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; cPND29.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT Modified-site 1 /label= Nle

FT Modified-site 2 /note= "bonded via N-terminal to polysaccharide- protein

FT Modified-site 2 /note= "epsilon-amino forms cyclic peptide with C-

FT Modified-site 11 /note= "D-Val; condenses with side chain NH2 of Lys(2) to

FT Modified-site give cyclic peptide"

XX
PN EP468714-A.

XX
PD 29-JAN-1992.

XX
PF 19-JUL-1990; 90US-00555558.

XX
PR 19-JUL-1990; 90US-00555558.

XX
PR 19-JUL-1990; 90US-00555974.

XX
PR 19-JUN-1991; 91US-00715275.

XX
PR 19-JUN-1991; 91US-00715277.

XX
PA (MERI) MERCK & CO INC.

XX
PI Marburg S, Tolman RL, Emini EA;

XX
XX WPI; 1992-034437/05.

XX
PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

XX
PT produce antibodies to prevent or treat HIV infection.

XX
PS Claim 9; Page 56; 63pp; English.
XX
CC The invention relates to a conjugate of an HIV principal neutralizing
CC determinant (PND), or an immunologically equivalent peptide (PEP),

CC covalently coupled to an immunogenic protein or protein complex through
CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
CC outer membrane protein complex (OMC) of *Neisseria meningitidis* b and the
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
CC The present sequence (CPND29) is an example of a PND peptide component.
CC The conjugates are used for inducing HIV-neutralising antibodies or for
CC making vaccines to prevent contraction of HIV infection or disease. The
CC antibodies can be used for passively protecting against infection by HIV,
CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays

XX
SQ Sequence 11 AA;

Query Match 43.7%; Score 31; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYPG 10
|||
Db 2 KHIGPG 7

RESULT 40
AAR95759
ID AAR95759 standard; peptide; 8 AA.
XX
AC AAR95759;
XX
DT 04-DEC-1996 (first entry)
XX
DE Alpha-4Beta-1 integrin binding inhibitory peptide 56.
XX
KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW inhibitor; binding; white blood cell; migration; capillary wall;
KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW CS1; CS5; H1; LDV; active site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8
FT /note= "Pro-NH2"
XX
PN USS510332-A.
XX
PD 23-APR-1996.
XX
PF 07-JUL-1994; 94US-00271830.
XX
PR 07-JUL-1994; 94US-00271830.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Beck PJ, Vanderslice P, Kogan TP, Ren K;
XX
DR WPI; 1996-221274/22.
XX
PT New peptide(s) based on the LDV domain of fibronectin - used for
PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or
PT invasin.
XX
PS Claim 4; Col 43-44; 35pp; English.
XX
CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
CC surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or VLA-
CC 4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white blood
CC cells flooding to the scene, causing widespread tissue damage. Cpts.

CC capable of blocking this process may be beneficial as therapeutic agents.
CC IA4B1 also recognises the extracellular matrix glycoprotein fibronectin.
CC Three distinct IA4B1-binding sites have been identified within
CC fibronectin. One site is found in the Hep1 region and is expressed in
CC all isoforms; two others (CS1 and CS5) are present in the alternatively
CC spliced type III connecting segments. CS1 has the higher affinity for
CC IA4B1 and contains the tripeptide LDV as its minimal active site.
CC Peptides AAR95704-805 are modeled after a portion of the CS1 peptide that
CC include the LDV domain presented in such a way by its novel flanking
CC sequence to produce a potent inhibitor of IA4B1 binding

XX
SQ Sequence 8 AA;

Query Match 42.3%; Score 30; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GPGW 11
|||
Db 1 GPGW 4

RESULT 41
ABP46859
ID ABP46859 standard; peptide; 8 AA.
XX
AC ABP46859;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv VH CDR3 SEQ ID 2870.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114759/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 2; Page 3068; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 8 AA;

Query Match 42.3%; Score 30; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GPGW 11
 |||||
 Db 2 GPGW 5

RESULT 42
 AAP95363
 ID AAP95363 standard; peptide; 9 AA.
 XX
 AC AAP95363;
 XX
 DT 30-MAR-1992 (first entry)
 XX
 DE Variable region V3, found in the envelope protein gp120 of an AIDS or ARC
 DE causing or related virus strain MAL.
 XX
 KW Vaccine; AIDS; ARC; HIV; diagnosis.
 XX
 OS AIDS virus.
 XX
 PN EP311219-A.
 XX
 PD 12-APR-1989.
 XX
 PF 07-OCT-1988; 88EP-00202248.
 XX
 PR 09-OCT-1987; 87NL-00002403.
 XX
 PA (DIER-) STICHTING CENT DIER.
 PA (UNAM) UNIV VAN AMSTERDAM.
 PA (UYAM-) UNIV AMSTERDAM ZIEKENHUI.
 XX
 PI Goudsmit J, Meloen RH;
 XX
 DR WPI; 1989-108193/15.
 XX
 PT Oligopeptide(s) corresp. to beta-turn variable region of gp.120 - used
 PT for diagnosis of and prodn of vaccines against AIDS and ARC.
 XX
 PS Disclosure; Page 4; 7pp; English.
 XX
 CC The peptides of the invention comprise the beta-turn AA SQ GPG or GPGR at
 CC positions 312-314 or 312-315 in the AA numbering of HTLV-IIIB (BH10) and
 CC flanking AA SQs having a length equal to or greater than 1 and pref.
 CC equal to or greater than 2 AAs; variants in which the GPG or GPGR SQ has
 CC been replaced by a different beta-turn SQ; and variants in which the free
 CC NH2-terminal gp AA and/or the free carboxyl terminal gp. AA has been
 CC blocked or modified otherwise
 XX
 SQ Sequence 9 AA;

Query Match 42.3%; Score 30; DB 1; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HYPG 10
 ||:||||

Db 2 HFGPG 6

RESULT 43
 AAR31288
 ID AAR31288 standard; peptide; 9 AA.
 XX
 AC AAR31288;
 XX
 DT 12-FEB-1993 (first entry)
 XX
 DE HIV principal determinant peptide.
 XX
 KW AIDS; ARC; human immunodeficiency virus; vaccine; Neisseria;
 KW meningitidis b; outer membrane protein complex; OMPC; PND-MAL.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "bonds to the OMPC of the conjugate via this site"

BP467700-A.
 XX
 PD 22-JAN-1992.
 XX
 PF 19-JUL-1991; 91EP-00306598.
 XX
 PR 19-JUL-1990; 90US-00555339.
 PR 19-JUL-1990; 90US-00555966.
 PR 19-JUN-1991; 91US-00715276.
 PR 19-JUN-1991; 91US-00715278.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Leanza WJ, Marburg S, Tolman RL, Emiri EA;
 XX
 DR WPI; 1992-026505/04.
 XX
 PT Conjugate proteins comprising HIV peptide components - useful for
 PT preparing vaccines for e.g. AIDS or for treating infections.
 XX
 PS Claim 12; Page 56; 63pp; English.
 XX
 CC The invention relates to a co-conjugate comprising an immunogenic protein
 CC or protein complex having a first set of covalent linkages to low
 CC molecular weight moieties which have an anionic or polyanionic character
 CC at physiological pH, and a second set of covalent linkages to peptides
 CC comprising HIV principal neutralizing determinants (PND's) or
 CC immunologically equivalent peptides. Preferably at least one set of the
 CC covalent linkages is comprised of maleimide derivatives; the
 CC (poly)anionic moiety is composed of one to five residues of the anionic
 CC form of a carboxylic, sulfonic or phosphonic acid; the immunogenic
 CC protein is the outer membrane protein complex (OMPC) of Neisseria
 CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
 CC bonded cyclic structure. The present sequence (PND-MAL) is an example of
 CC a PND peptide component used in the co-conjugate. The co-conjugate is
 CC useful for inducing anti-peptide immune response in mammals, for inducing
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
 CC prevent HIV infection or disease, including AIDS, or for treating humans
 CC afflicted with HIV infection or disease
 XX
 SQ Sequence 9 AA;

Query Match 42.3%; Score 30; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HYPG 10
 ||:||||
 Db 2 HFGPG 6

RESULT 44
ID AAR30043 standard; peptide; 9 AA.
XX AAR30043;
AC AAR30043;
XX 25-MAR-2003 (revised)
DT 28-APR-1993 (first entry)
XX
DE HIV principle neutralising determinant MAL.
XX
KW Human immunodeficiency virus; AIDS; PND; MIEP; conjugate;
KW major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen;
KW passive immunisation.
XX
OS Human immunodeficiency virus.
XX
PN EP519554-A1.
XX
PD 23-DEC-1992.
XX
PF 11-JUN-1992; 92EP-00201693.
XX
PR 19-JUN-1991; 91US-00715273.
XX
PA (MERI) MERCK & CO INC.
XX
PI Emini A, Liu MA, Marburg S, Tolman RL;
XX
DR WPI; 1992-425771/52.
XX
PT Conjugates of HIV-1 PND peptide(s) with the MIEP of Neisseria
PT meningitidis - useful as a vaccine for treating and preventing HIV-1
PT infection, e.g. AIDS in humans.
XX
PS Claim 9; Page 60; 66pp; English.
XX
CC The peptide is HIV principle neutralising determinant (PND) MAL and is
CC used as part of a conjugate comprising the major immune enhancing protein
CC (MIEP) of Neisseria meningitidis covalently linked to the HIV PND. The
CC conjugate may be used to prepare vaccines against HIV infections, e.g.
CC AIDS, as research tools for studying PND structure- function
CC relationships, or as immunogens for use in the passive immunisation of
CC humans. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 42.3%; Score 30; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 HYGPG 10
|:|
|:|
|:|
Db 2 HFGPG 6
RESULT 45
ID AAR26724 standard; peptide; 9 AA.
XX AAR26724;
AC AAR26724;
XX 09-FEB-1993 (first entry)
DT
XX
DE HIV-PND-polysaccharide-protein conjugate vaccine.
XX
KW Human immunodeficiency virus; principal neutralizing determinant;
KW outer membrane protein complex; OMPC; Neisseria; AIDS; PND-MAL.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers

FT Modified-site 1 /note= "Joins onto polysaccharide-protein complex via
FT this site"
FT
XX EP468714-A.
XX
PN 29-JAN-1992.
XX
PD 19-JUL-1990; 90US-00555558.
XX
PF 19-JUL-1990; 90US-00555558.
XX
PR 19-JUL-1990; 90US-00555558.
PR 19-JUN-1991; 91US-00715275.
PR 19-JUN-1991; 91US-00715277.
XX
PA (MERI) MERCK & CO INC.
XX
PI Marburg S, Tolman RL, Emini EA;
XX
DR WPI; 1992-034437/05.
XX
PT HIV peptide-polysaccharide-protein conjugates - used in vaccines or to
PT produce antibodies to prevent or treat HIV infection.
XX
PS Claim 9; Page 57; 63pp; English.
XX
CC The invention relates to a conjugate of an HIV principal neutralizing
CC determinant (PND), or an immunologically equivalent peptide (PP),
CC covalently coupled to an immunogenic protein or protein complex through
CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
CC The present sequence (PND-MAL) is an example of a PND peptide component.
CC The conjugates are used for inducing HIV-neutralising antibodies or for
CC making vaccines to prevent contraction of HIV infection or disease. The
CC antibodies can be used for passively protecting against infection by HIV,
CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays
XX
SQ Sequence 9 AA;
Query Match 42.3%; Score 30; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 HYGPG 10
|:|
|:|
|:|
Db 2 HFGPG 6
Search completed: August 30, 2004, 10:49:31
Job time : 18.3885 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 10.5912 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-6
Perfect score: 63
Sequence: 1 IYGERPPDENF 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29	46.0	13	4	Q9UPE7	Q9UPE7 homo sapien
2	23	36.5	14	2	P96350	P96350 Legionella
3	22	34.9	11	2	Q48933	Q48933 mycobacteri
4	22	34.9	14	11	Q9JUJ5	Q9JUJ5 mus musculu
5	20	31.7	10	2	P96352	P96352 marinobacte
6	20	31.7	10	2	Q93LE5	Q93LE5 photobacter
7	20	31.7	10	2	P96321	P96321 escherichia
8	20	31.7	10	2	P96306	P96306 aeromonas s
9	20	31.7	13	13	Q8UJ32	Q8UJ32 ficedula al
10	20	31.7	13	13	Q9PS56	Q9PS56 carassius a
11	20	31.7	14	4	Q7Z5S0	Q7Z5S0 homo sapien
12	19	30.2	13	4	Q8WY56	Q8WY56 homo sapien
13	18	28.6	10	2	Q8KHN9	Q8KHN9 clostridium
14	18	28.6	10	4	Q7Z5A2	Q7Z5A2 homo sapien
15	18	28.6	10	8	Q85V65	Q85V65 eucalyptus
16	18	28.6	10	11	Q9QVF7	Q9QVF7 rattus sp.

17	18	28.6	10	11	Q63389	Q63389 rattus norv
18	18	28.6	10	11	Q9QVF1	Q9QVF1 mus sp. pro
19	18	28.6	11	2	O87882	O87882 mycobacteri
20	18	28.6	13	4	Q9UNV6	Q9UNV6 homo sapien
21	18	28.6	14	2	Q52840	Q52840 rhizobium l
22	18	28.6	14	2	Q52636	Q52636 escherichia
23	17	27.0	8	2	Q7X139	Q7X139 staphylococ
24	17	27.0	8	13	Q90ZV5	Q90ZV5 fulica leuc
25	17	27.0	9	11	Q62530	Q62530 mus spretus
26	17	27.0	10	2	Q48469	Q48469 klebsiella
27	17	27.0	10	2	P96305	P96305 alteromonas
28	17	27.0	10	4	Q9UN90	Q9UN90 homo sapien
29	17	27.0	10	16	P96423	P96423 pseudomonas
30	17	27.0	12	2	Q8GMM8	Q8GMM8 acinetobact
31	17	27.0	13	11	Q9CU06	Q9CU06 mus musculu
32	16	25.4	8	10	O8GTG5	O8GTG5 lycopersico
33	16	25.4	11	2	Q47604	Q47604 escherichia
34	16	25.4	11	3	Q9HFN8	Q9HFN8 candida rug
35	16	25.4	11	5	Q9UAR8	Q9UAR8 aedes aegyp
36	16	25.4	11	6	Q9TRW5	Q9TRW5 bos taurus
37	16	25.4	11	13	Q7T285	Q7T285 geochelone
38	16	25.4	11	13	Q7T284	Q7T284 geochelone
39	16	25.4	11	13	Q7T283	Q7T283 geochelone
40	16	25.4	11	13	Q7SX72	Q7SX72 geochelone
41	16	25.4	11	13	Q7SX71	Q7SX71 geochelone
42	16	25.4	11	15	Q9DZ32	Q9DZ32 human immun
43	16	25.4	12	4	Q8IVH0	Q8IVH0 homo sapien
44	16	25.4	12	10	Q9S8F0	Q9S8F0 zea mays (m
45	16	25.4	12	12	Q88577	Q88577 theiler's e

ALIGNMENTS

RESULT 1	ID	Q9UPE7	PRELIMINARY;	PRT;	13 AA.
AC	Q9UPE7				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)				
DE	Inosine monophosphatase 2 (Fragment).				
GN	IMPA2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97463449; PubMed=9322233;				
RA	Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,				
RA	Detera-Wadleigh S.D.;				
RT	"A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a				
RT	susceptibility region for bipolar disorder.";				
RL	Mol. Psychiatry 2:393-397(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20284187;				
RA	Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,				
RA	Esterling L.E., Detera-Wadleigh S.D.;				
RT	"Genomic structure and novel variants of myo-inositol monophosphatase				
RT	2.";				
RL	Mol. Psychiatry 5:165-171(2000).				
DR	EMBL; AF025882; AAD22136.1; -				
DR	EMBL; AF025881; AAD22136.1; JOINED.				
FT	NON_TER	1			
FT	NON_TER	1			
FT	NON_TER	1			
SO	SEQUENCE	13 AA;	1589 MW;	F3415D841F48D401 CRC64;	
Query Match		46.0%;	Score 29;	DB 4;	Length 13;
Best Local Similarity		62.5%;	Pred. No. 1.5e+02;		
Matches	5;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;

QY 4 ERFPDENF 11
| | | | |
Db 1 ERFPDENF 8

RESULT 2

P96350 PRELIMINARY; PRT; 14 AA.

AC P96350;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
GN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68079; AAB48026.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1349 MW; CE5F7318D3BE7D7D CRC64;

Query Match 36.5%; Score 23; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
| | | | |
Db 3 DENF 6

RESULT 3

Q48933 PRELIMINARY; PRT; 11 AA.

AC Q48933; P77701; Q48932; 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, last sequence update)
DT 01-NOV-1996 (TRENBLREL. 01, last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, last annotation update)
DE Alkyl hydroperoxide reductase C (Fragment).
GN AHPC.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35728, and ATCC35727;
RA Zhang Y., Derecic V.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC35735;
RX MEDLINE=96256622; PubMed=8655566;
RA Dhandayuthapani S., Zhang Y., Derecic V.;
RT "Oxidative stress response and its role in sensitivity to isoniazid in
RT Mycobacterium smegmatis and lack of expression in M. aurum and M.
RT tuberculosis."
RT J. Bacteriol. 178:3641-3649(1996).
RL EMBL; U58031; AAB00320.1; -.
DR EMBL; U57979; AAA99830.1; -.
DR EMBL; U57978; AAA99829.1; -.
DR EMBL; U57762; AAB00317.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 34.9%; Score 22; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7
| : | | |
Db 7 GDQFP 11

RESULT 4

Q9JUU5 PRELIMINARY; PRT; 14 AA.

AC Q9JUU5;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
DE B-Raf protein (Fragment).
GN B-RAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Barnier J.V.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Barnier J.V., Papin C., Bychene A., Lecog O.;
RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-
RT specific expression."
RL J. Biochem. 270:23389(1995).
DR EMBL; AJ276308; CAB81556.1; -.
FT NON TER 1
FT NON TER 14
SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 34.9%; Score 22; DB 11; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERFPD 8
| : | | |
Db 2 EKFPD 6

RESULT 5

P96352 PRELIMINARY; PRT; 10 AA.

AC P96352;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Marinobacter hydrocarbonasticus (Pseudomonas nautica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
OX NCBI_TaxID=2743;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 49840;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68077; AAB48027.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11

Db 3 DENY 6

RESULT 6

Q93LE5 PRELIMINARY; PRT; 10 AA.
AC Q93LE5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213;
RA Williams K.P.;
RL "The tmRNA website."
RN Nucleic Acids Res. 28:168-168(2000).
[2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RT "Phylogenetic analysis of tmRNA."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040837; AAK83525.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
Db 3 DENY 6

RESULT 7

P96321 PRELIMINARY; PRT; 10 AA.
AC P96321;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023883; PubMed=7524073;
RA Komine Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from
RT Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68074; AAB48024.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
Db 3 DENY 6

RESULT 8

P96306 PRELIMINARY; PRT; 10 AA.
AC P96306;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33658;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68075; AAB48022.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
Db 3 DENY 6

RESULT 9

O8UJ32 PRELIMINARY; PRT; 13 AA.
AC O8UJ32;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE 37LRP/p40 (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome."
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454232; AAM22911.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;

Query Match 31.7%; Score 20; DB 13; Length 13;
Best Local Similarity 44.4%; Pred. No. 7e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IYGERFPDE 9
Db 5 LYFYRDPDE 13

RESULT 10

Q9PS56 PRELIMINARY; PRT; 13 AA.
AC Q9PS56; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE NEUROLIN=CELL surface glycoprotein (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE.
RX MEDLINE=92250720; PubMed=1577862;
RA Paschke K.A., Lottspeich F., Stuenkel C.A.;
RT "Neurolin, a cell surface glycoprotein on growing retinal axons in the goldfish visual system, is reexpressed during retinal axonal regeneration.";
RL J. Cell Biol. 117:863-875(1992).
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1332 MW; 33AF8FF8CC535728 CRC64;

Query Match 31.7%; Score 20; DB 13; Length 13;
Best Local Similarity 75.0%; Pred. No. 7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYGE 4
Db 7 LYGE 10

RESULT 11

Q7Z5S0 PRELIMINARY; PRT; 14 AA.
ID Q7Z5S0;
AC Q7Z5S0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RA "generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054509; AAH54509.1; -
KW Hypothetical protein.
SQ SEQUENCE 14 AA; 1893 MW; 5A6D6F30E6465257 CRC64;

Query Match 31.7%; Score 20; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IYGER 5
Db 7 LYGER 11

RESULT 12

Q8WY56 PRELIMINARY; PRT; 13 AA.
ID Q8WY56;
AC Q8WY56;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Epithelial sodium channel beta-3 subunit (Fragment).
GN SCN1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;
RT "Genomic organization of the 5' end of human beta ENaC and preliminary characterization of its promoter.";
RL Am. J. Physiol. Renal Physiol. 0:0-0(2002).
DR EMBL; AF260228; AAL48197.1; -
DR GO; GO:0005216; Filion channel activity; IEA.
KW Ionic channel.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;

Query Match 30.2%; Score 19; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
Db 9 DXNF 12

RESULT 13

Q8KHN9 PRELIMINARY; PRT; 10 AA.
ID Q8KHN9;
AC Q8KHN9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE BONT/A (Fragment).
GN BONT/A.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=62A, and NCTC 2916;
RA Dineen S.S., Bradshaw M., Johnson E.A.;
RT "Comparison of the neurotoxin gene clusters in Clostridium botulinum type A strains.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461539; AAM75954.1; -
DR EMBL; AF461541; AAM75962.1; -
FT NON_TER 1
FT NON_TER 1

SQ SEQUENCE 10 AA; 1143 MW; 8721FA0B1863787A CRC64;

Query Match 28.6%; Score 18; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGER 5

DB 5 WGER 8

RESULT 14

ID Q7Z5A2 PRELIMINARY; PRT; 10 AA.

AC Q7Z5A2; 01-OCT-2003 (TReMBLrel. 25, Created)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Fraisl P., Forss-Petter S., Berger J.;

RT "A novel relative of Bubblegum."

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AU577571; CAB2153.1; -.

KW Hypothetical protein.

SQ SEQUENCE 10 AA; 1086 MW; 622094D8786769D4 CRC64;

Query Match 28.6%; Score 18; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFP 7

DB 3 RFP 5

RESULT 15

ID Q85V65 PRELIMINARY; PRT; 10 AA.

AC Q85V65; 01-JUN-2003 (TReMBLrel. 24, Created)

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Ribosomal protein L2 (Fragment).

OS Eucalyptus grandis (Floccod gum).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Myrtales; Myrtaceae; Eucalyptus.

OX NCBI_TaxID=71139;

RN [1]

RP SEQUENCE FROM N.A.

RA Jones M.E., Shepherd M., Henry R.J., Delves A., Schoer L.;

RT "Intraspecific chloroplast DNA variation and population structure in

RT Eucalyptus grandis revealed by single-strand conformation polymorphism

RT (SSCP)."

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF502121; AAP30826.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

KW Chloroplast; Ribosomal protein.

FT NON TER 1

SQ SEQUENCE 10 AA; 1205 MW; 5387F0140879C057 CRC64;

Query Match 28.6%; Score 18; DB 8; Length 10;

Best Local Similarity 60.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGER 5

DB 4 IFGRR 8

RESULT 16

ID Q9QVF7 PRELIMINARY; PRT; 10 AA.

AC Q9QVF7; 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE.

RX MEDLINE=92135065; PubMed=1777418;

RA Matsuda T., Koike T.;

RA Yasuda T., Koike T.;

RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by

RT cDNA cloning and inter-species differences of beta 2-GPI in

RT alternation of anticardiolipin binding."

RL Int. Immunol. 3:1217-1221(1991).

FT NON TER 1

FT NON TER 1

SQ SEQUENCE 10 AA; 1100 MW; 94E681B767376EA1 CRC64;

Query Match 28.6%; Score 18; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9

DB 7 PDE 9

RESULT 17

ID Q63389 PRELIMINARY; PRT; 10 AA.

AC Q63389; 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Ornithine decarboxylase (ODC).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Testis;

RX MEDLINE=89255378; PubMed=2722815;

RA Wen L., Huang J.K., Blackshear P.J.;

RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential

RT regulatory elements, and comparison to the mouse gene."

RL J. Biol. Chem. 264:9016-9021(1989).

DR EMBL; J04791; AAA66163.1; -.

DR PIR; B33710; B33710.

SQ SEQUENCE 10 AA; 1074 MW; 30F6E69D415BDC7 CRC64;

Query Match 28.6%; Score 18; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFP 7

DB 6 RFP 8

RESULT 18

Q9QVF1 PRELIMINARY; PRT; 10 AA.
 AC Q9QVF1; 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Protamine MP2 (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92174934; PubMed=1541289;
 RA Chauviere M., Martinge A., Debatte M., Sauriere P., Chevallier P.;
 RT "Molecular characterization of six intermediate proteins in the
 RL processing of mouse protamine P2 precursor.";
 RL Eur. J. Biochem. 204:759-765(1992).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1280 MW; 01DD2975A406841B CRC64;

Query Match 28.6%; Score 18; DB 11; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGERPDE 9
 DB 3 YMRSPSE 10

RESULT 19

087882 PRELIMINARY; PRT; 11 AA.
 AC 087882;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE Alkyl hydroperoxide reductase (Fragment).
 GN AHPC.
 OS Mycobacterium xenopi.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1789;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19250;
 RX MEDLINE=98406038; PubMed=9733688;
 RA Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deretic V.;
 RT "Oxidative stress response and characterization of the oxyR-ahpc and
 RT furA-katG loci in Mycobacterium marinum.";
 RL J. Bacteriol. 180:4856-4864(1998).
 DR EMBL; U43810; AAC61663.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1147 MW; 45458CE1787041A7 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERFP 7
 DB 7 GGQFP 11

RESULT 20

Q9UNV6 PRELIMINARY; PRT; 13 AA.
 AC Q9UNV6;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Inosine monophosphatase 2 (Fragment).
 GN IMPA2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97463449; PubMed=9322233;
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
 RA Detera-Wadleigh S.D.;
 RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
 RT susceptibility region for bipolar disorder.";
 RL Mol. Psychiatry 2:393-397(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20284187;
 RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
 RA Esterling L.E., Detera-Wadleigh S.D.;
 RT "Genomic structure and novel variants of myo-inositol monophosphatase
 RT 2.";
 RL Mol. Psychiatry 5:165-171(2000).
 DR EMBL; AF085628; AAD22141.1; -.
 DR EMBL; AF085627; AAD22141.1; JOINED.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 28.6%; Score 18; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFP 7
 DB 7 RFP 9

RESULT 21

Q52840 PRELIMINARY; PRT; 14 AA.
 AC Q52840;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE Homology with C-terminus of other Rhizobium nodB genes.
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Mesorhizobiaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97002748; PubMed=8850088;
 RA Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,
 RA Rockman E.S., Lewis P.E., Pankhurst C.E.;
 RT "Novel and complex chromosomal arrangement of Rhizobium loti
 RT nodulation genes.";
 RL Mol. Plant Microbe Interact. 9:187-197(1996).
 DR EMBL; L06241; AAB47352.1; -.
 SQ SEQUENCE 14 AA; 1600 MW; 90C26EC32C8F34C5 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFP 7
 DB 9 RFP 11

RESULT 22

Q52636 PRELIMINARY; PRT; 14 AA.
 ID Q52636

AC Q52636;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tral protein (Fragment).
GN TRAL.
OS Escherichia coli.
OG Plasmid R124.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86059219; PubMed=2999074;
RA Frost L.S., Finlay B.B., Opgenorth A., Paranchych W., Lee J.S.;
RT "Characterization and sequence analysis of pilin from F-like
RT plasmids."
RL J. Bacteriol. 164:1238-1247(1985).
DR EMBL; K03092; AAA92759.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 14 AA; 1713 MW; 5CCA91188EB30E23 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFP 7
Db 12 RFP 14

RESULT 23
07X139 PRELIMINARY; PRT; 8 AA.
AC 07X139;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SecE (Fragment).
OS Staphylococcus cohnii.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=29382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GIFU9122;
RA Morikawa K., Inose Y., Ohta T.;
RT "A new Staphylococcal sigma factor in the conserved gene cassette:
RT Functional significance and implication for the evolutionary
RT processes."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY234840; AAO62607.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 1014 MW; F0C9C4B13333DD6 CRC64;

Query Match 27.0%; Score 17; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ENF 11
Db 5 ENF 7

RESULT 24
Q90ZV5 PRELIMINARY; PRT; 8 AA.
AC Q90ZV5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Adenylate kinase (Fragment).

OS Fulica leucoptera.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
OX NCBI_TaxID=156758;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapero L.H., Dumbacher J.P.;
RT "Adenylate kinase intron 5: a new nuclear locus for avian
RT systematics."
RL Auk 118:248-255(2001).
DR EMBL; AF307898; AAK43537.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 27.0%; Score 17; DB 13; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERF 6
Db 2 GERF 5

RESULT 25
Q62530 PRELIMINARY; PRT; 9 AA.
AC Q62530;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone
DE GLA-protein) (BGP) (Fragment).
GN BGLAP1.
OS Mus spretus (western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maizaki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
RL Mamm. Genome 5:349-355(1994).
CC -1- FUNCTION: THIS BONE PROTEIN, CONSTITUTES 1-2% OF THE TOTAL PROTEIN
CC -1- OF BONE. IT BINDS STRONGLY TO APATITE AND CALCIUM.
CC -1- TISSUE SPECIFICITY: BONE.
CC -1- PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN K
CC DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
CC BINDING OF CALCIUM.
DR EMBL; U05695; AAB60465.1; -.
DR PIR; I49406; I49406.
DR MGD; MGI:88156; Bglap1.
FT NON_TER
SQ SEQUENCE 9 AA; 1135 MW; 5937E0586B504403 CRC64;

Query Match 27.0%; Score 17; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3
Db 4 IYG 6

RESULT 26
Q48469 PRELIMINARY; PRT; 10 AA.
AC Q48469;
AC Q48469;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nitrogenase (Fragment).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S.C., Xue Z.T., Kong Q.T., Wu Q.L.;
RT "An open reading frame upstream from the rnfH gene of Klebsiella pneumoniae."
RL Nucleic Acids Res. 11:4241-4250(1983).
DR EMBL; X01006; CAA25501.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1173 MW; B130695DDEA6CA06 CRC64;

Query Match 27.0%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3
DB 8 IYG 10

RESULT 27
P96305 PRELIMINARY; PRT; 10 AA.
ID P96305;
AC P96305;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Alteromonas haloplanktis (Pseudoalteromonas haloplanktis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Pseudoalteromonas.
OX NCBI_TaxID=228;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 14393;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68076; AAB48021.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1053 MW; 857BD235AB54AAA CRC64;

Query Match 27.0%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
DB 3 DDNY 6

RESULT 28
Q9UN90 PRELIMINARY; PRT; 10 AA.
ID Q9UN90;
AC Q9UN90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Canalicular multispecific organic anion transporter (Fragment).
GN CMOAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka T., Uchiyama T., Hinochita E., Inokuchi A., Toh S., Wada M.,
RA Nomoto M., Kohno K., Kuwano M.;
RT "Sequence analysis and functional characterization of the 5'-flanking region of the human canalicular multispecific organic anion transporter/multidrug resistance protein 2 (CMOAT/MRP2) gene."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144630; AAD47599.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1219 MW; 76F28CB44EB9C3B CRC64;

Query Match 27.0%; Score 17; DB 4; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
DB 3 EKFCNSTF 10

RESULT 29
P96423 PRELIMINARY; PRT; 10 AA.
ID P96423;
AC P96423;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Coded portion of proteolysis tag (Translated portion of tmRNA gene ssra) (Fragment).
GN PA0826.1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 25330;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; U68078; AAB48029.1; -.
DR EMBL; AE004517; AAO42616.1; -.
KW Complete proteome.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1037 MW; 857BD22DCB54AAA CRC64;

Query Match 27.0%; Score 17; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
DB 3 DDNY 6

RESULT 30
Q8GMM8 PRELIMINARY; PRT; 12 AA.
ID Q8GMM8

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AC Q8GMB8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Transposase (Fragment).
GN TNPI006.
OS Acinetobacter sp. BW3.
OG Plasmid pKLH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKLH207;
RA Kholodil G.Y., Yurleva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3; PLASMID=pKLH207;
RA Kholodil G.Y., Mindlin S.Z., Gorlenko Z.M., Yurleva O.V.,
RA Petrova M.A., Nikiforov V.G.;
RT "A young family of transposable adaptive DNA segments identified in
RT the Acinetobacter genus.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250234; CAC80781.1; -.
DR EMBL; AJ486856; CAD31077.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1457 MW; E5832A70F8F40871 CRC64;

Query Match 27.0%; Score 17; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 2.3e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGERFPDE 9
Db 5 HGRHFGGE 12

RESULT 31
Q9CU06 PRELIMINARY; PRT; 13 AA.
AC Q9CU06;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Zona pellucida binding protein (Fragment).
GN ZPBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK018876; BAB31470.1; -.
DR MGD; MGI:1855701; Zpdp.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1404 MW; D6A4220999576B42 CRC64;

Query Match 27.0%; Score 17; DB 11; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGER 5
Db 6 VYGAX 10

RESULT 32
Q8GTG5 PRELIMINARY; PRT; 8 AA.
AC Q8GTG5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE WRKY transcription factor Iid-1 splice variant 2 (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Money Maker; TISSUE=Leaf;
RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somsich I.E.;
RT "Comparison of WRKY group II transcription factors from plants.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157059; AAN71729.1; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 917 MW; 59177B4775B87330 CRC64;

Query Match 25.4%; Score 16; DB 10; Length 8;
Best Local Similarity 42.9%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGERFP 7
Db 1 IKGSPYP 7

RESULT 33
Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Rease protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375 (1991).

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DR EMBL; M63621; AAA24560.1; -.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 25.4%; Score 16; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.2e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDEN 10
 DB 4 PDLN 7

RESULT 34

Q9HFN8

ID Q9HFN8 PRELIMINARY; PRT; 11 AA.

AC Q9HFN8; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

OS Acyl carrier protein (Fragment).

GN ACP.

OC Candida rugosa (Yeast) (Candida cylindracea).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=5481;

RN [1]

RP SEQUENCE FROM N.A.

RA Biasio W.; Thesis (2000), University of Vienna, Austria.

RL EMBL; AJ279021; CAC08612.1; -.

DR NON_TER 1

SQ SEQUENCE 11 AA; 1274 MW; D2E4CC3976C40732 CRC64;

Query Match 25.4%; Score 16; DB 3; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.2e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGERPD 8
 DB 3 YVLRPD 9

RESULT 35

Q9UAR8

ID Q9UAR8 PRELIMINARY; PRT; 11 AA.

AC Q9UAR8; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OS Stalokinin I preproprotein (Fragment).

OC Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

OX NCBI_TaxID=7159;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;

RX MEDLINE=20099025; PubMed=10620041;

RT Beerntsen B.T.; Champagne D.E.; Coleman J.L.; Campos Y.A.; James A.A.;

RT "Characterization of the Stalokinin I gene encoding the salivary

RT vasodilator of the yellow fever mosquito, Aedes aegypti.";

RL Insect Mol. Biol. 8:459-467(1999).

DR EMBL; AF108100; AAD16884.1; -.

DR GO; GO:0007268; P:synaptic transmission; IEA.

DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.

DR InterPro; IPR002040; Tachy Neurokinin.

DR PROSITE; PS00267; TACHYKININ; 1.

FT NON_TER 1

SQ SEQUENCE 11 AA; 1203 MW; 8BADC77C6B59C33A CRC64;

Query Match 25.4%; Score 16; DB 5; Length 11;
 Best Local Similarity 50.0%; Pred. No. 3.2e+04;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERF 6
 DB 3 GDXF 6

RESULT 36

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.

AC Q9TRW5; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS 25 kDa protein p25, peptide F4 (Fragment).

OC Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=91372400; PubMed=1909972;

RA Takahashi M.; Tomizawa K.; Ishiguro K.; Sato K.; Omori A.; Sato S.;

RA Shiratsuchi A.; Uchida T.; Imahori K.;

RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a

RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";

RL FEBS Lett. 289:37-43(1991).

FT NON_TER 1

SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 25.4%; Score 16; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
 DB 2 ERF 4

RESULT 37

Q7T285

ID Q7T285 PRELIMINARY; PRT; 11 AA.

AC Q7T285; 01-OCT-2003 (TREMBlrel. 25, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Creatine kinase (Fragment).

OC Geophilone carbonaria (Red-footed tortoise).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Testudines; Cryptodira; Testudinidae; Testudinidae; Geophilone.

OX NCBI_TaxID=50047;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=red; Burns C.; Sezzi E.; Bergman W.; Powell J.R.; Caccione A.;

RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in

RT the Giant Galapagos Tortoise.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY101746; AAM34549.1; -.

KW Kinase.

FT NON_TER 1

FT NON_TER 11

SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 25.4%; Score 16; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
 DB 3 ERF 5

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RESULT 38
Q7T284 PRELIMINARY; PRT; 11 AA.
ID Q7T284
AC Q7T284;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone denticulata (Yellow footed tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=101697;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=yellow2;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101747; AAM34550.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

RESULT 39
Q7T283 PRELIMINARY; PRT; 11 AA.
ID Q7T283
AC Q7T283;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone pardalis (leopard tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=55540;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=to;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101748; AAM34551.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

RESULT 40
Q7SX72 PRELIMINARY; PRT; 11 AA.
ID Q7SX72

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AC Q7SX72;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone chilensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=106216;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1864, and 8136;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101744; AAM34547.1; -.
DR EMBL; AY101745; AAM34548.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

RESULT 41
Q7SX71 PRELIMINARY; PRT; 11 AA.
ID Q7SX71
AC Q7SX71;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone nigra (Galapagos giant tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=66189;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AGOL, CAZ22, CRU1, ESPL, IG, ME4, PB3, P244, PZ6, and VA935;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101734; AAM34537.1; -.
DR EMBL; AY101735; AAM34538.1; -.
DR EMBL; AY101736; AAM34539.1; -.
DR EMBL; AY101737; AAM34540.1; -.
DR EMBL; AY101738; AAM34541.1; -.
DR EMBL; AY101739; AAM34542.1; -.
DR EMBL; AY101740; AAM34543.1; -.
DR EMBL; AY101741; AAM34544.1; -.
DR EMBL; AY101742; AAM34545.1; -.
DR EMBL; AY101743; AAM34546.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 25.4%; Score 16; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
DB 3 ERF 5

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RESULT 42

Q9DZ32
ID Q9DZ32 PRELIMINARY; PRT; 11 AA.
AC Q9DZ32;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE Gag polypeptide (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., Depasquale M.P., Kartsonis N., Hanna G.J.,
Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savaia A.,
Petroopoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
Siliciano R., D'Aquila R.T.;
RA "Antiretroviral resistance during successful therapy of HIV type 1
infection";
RT Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953 (2000).
DR EMBL: AF292799; AAG25407.1; -.
KW Polypeptide.
FT NON TER 1
SQ SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 25.4%; Score 16; DB 15; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 RFPDE 9
Db 4 RTPNE 8

RESULT 43

Q8IVH0
ID Q8IVH0 PRELIMINARY; PRT; 12 AA.
AC Q8IVH0;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Truncated PAX6 protein (Fragment).
GN PAX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Neethirajan G., Krishnas S.R., Vijayalakshmi P., Sundaresan P.;
RT "Mutation analysis in Human PAX6 gene of Aniridia";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF548390; AAN86817.1; -.
FT NON TER 1
SQ SEQUENCE 12 AA; 1511 MW; 9E169541A67B51F1 CRC64;

Query Match 25.4%; Score 16; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 FPD 8
Db 7 YPD 9

RESULT 44

Q9S8F0
ID Q9S8F0 PRELIMINARY; PRT; 12 AA.
AC Q9S8F0;

DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.18) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RX MEDLINE=95322859; PubMed=7599527;
RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,
Greenland A.J.;
RA "Characterization of the safener-induced glutathione S-transferase
isoform II from maize";
RT Planta 196:295-302 (1995).
DR GO: 0004364; F: glutathione transferase activity; IEA.
SQ SEQUENCE 12 AA; 1382 MW; C28977F65975B05D CRC64;

Query Match 25.4%; Score 16; DB 10; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYG 3
Db 1 VYG 3

RESULT 45

Q88577
ID Q88577 PRELIMINARY; PRT; 12 AA.
AC Q88577;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO(4);
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence";
RL J. Virol. 66:1951-1958 (1992).
DR EMBL: M80885; AAA73156.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 25.4%; Score 16; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 FPD 8
Db 7 YPD 9

Search completed: August 30, 2004, 10:55:24
Job time : 13.5912 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.89527 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469a-6
Perfect score: 63
Sequence: 1 IYGERFPDENF 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	25	39.7	10 1	SLAP_BACTG P49325 bacillus th
2	23	36.5	10 1	URAY_HUMAN P34990 homo sapien
3	21	33.3	11 1	COXA_CANFA P99501 canis fam11
4	21	33.3	11 1	TKM4_PSEGU P42989 pseudophryn
5	21	33.3	12 1	FR1_SABU P83349 sarcophaga
6	20	31.7	10 1	FAR7_MACRS P83280 macrobrachi
7	20	31.7	14 1	LPER_BACLI Q04303 bacillus 11
8	19	30.2	8 1	FAR2_MACRS P83275 macrobrachi
9	19	30.2	9 1	FAR3_MACRS P83276 macrobrachi
10	19	30.2	11 1	EFG_CLOPA P81350 clostridium
11	18	28.6	8 1	FAR1_PENMO P83316 penaeus mon
12	18	28.6	8 1	FAR3_HOMAM P41486 homarus ame
13	18	28.6	9 1	UPA3_HUMAN P30089 homo sapien
14	18	28.6	10 1	PNEU_RAT P21996 rattus norv
15	18	28.6	10 1	RT02_BOVIN P82923 bos taurus
16	18	28.6	11 1	TKN1_PSEGU P42986 pseudophryn
17	18	28.6	11 1	TKN1_UPERU P08612 uperoleia r
18	18	28.6	11 1	TKN2_PSEGU P42987 pseudophryn
19	18	28.6	12 1	PSR3_PHYPA P08662 physcomitre
20	18	28.6	13 1	NP3_LYMTS P80180 lymanaea sta
21	18	28.6	13 1	PSBP_PINPS P81668 pinus pinas
22	18	28.6	14 1	MARI_ALTSP P29399 alteromonas
23	17	27.0	8 1	FAR1_PANRE P41872 panagrellus
24	17	27.0	9 1	FAR2_PANRE P41873 panagrellus
25	17	27.0	9 1	FAR4_CALVO P41859 calliphora
26	17	27.0	10 1	UPA8_HUMAN P30094 homo sapien
27	17	27.0	11 1	LSK1_LEUMA P04428 leucophaea
28	17	27.0	11 1	LSKP_PERAM P36885 periplaneta
29	17	27.0	13 1	ADFB_TENMO P83109 tenebrio mo
30	17	27.0	14 1	NSK2_SABU P41493 sarcophaga
31	17	27.0	14 1	TKN1_SCHGR P82470 schistocerc
32	17	27.0	14 1	UC04_MAIZE P80610 zea mays (m
33	16	25.4	8 1	ALU1_CYDPO P82152 cydia pomon

34	16	25.4	8 1	FAR7_ASCSU P43171 ascaris suu
35	16	25.4	9 1	FAR1_CALVO P41856 calliphora
36	16	25.4	9 1	FAR2_CALVO P41857 calliphora
37	16	25.4	9 1	FAR3_CALVO P41858 calliphora
38	16	25.4	9 1	FRP1_SABU P83350 sarcophaga
39	16	25.4	9 1	TKC1_CALVO P41517 calliphora
40	16	25.4	9 1	TKL1_LOCM1 P16223 locusta mig
41	16	25.4	10 1	PORB_METTM P80901 methanobact
42	16	25.4	10 1	PPOK_FASHE P80525 fasciola he
43	16	25.4	10 1	TKL2_LOCM1 P16224 locusta mig
44	16	25.4	10 1	TKL3_LOCM1 P30249 locusta mig
45	16	25.4	10 1	TKS1_AEDAE P42634 aedes aegyp

ALIGNMENTS

RESULT 1
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckevich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
of proteins which coat the surface of bacteria.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH OBLIQUE (P2) SYMMETRY.
CC PIR; A60476; A60476.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECAACAB769D1A3 CRC64;

Query Match 39.7%; Score 25; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GERFPD 8
Db 2 GKTFPD 7

RESULT 2

URAY_HUMAN STANDARD; PRT; 10 AA.
ID URAY_HUMAN
AC P34990;

DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Erythrocyte;
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochstrasser D.F.;
RL Submitted (FEB-1994) to Swiss-Prot.

CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.77, its MW is: 26 Kda.
 DR SWISS-2DPAGE; P34990; HUMAN.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match 36.5%; Score 23; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 YGERFPD 8
 :|||
 Db 3 HGENFXD 9

RESULT 3

COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins."
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 DR HSC-2DPAGE; P99501; DOG.
 DR InterPro; IPR003204; Cyt_c_ox5A.
 DR Pfam; PF02284; COX5A; 1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB1F5 CRC64;

Query Match 33.3%; Score 21; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 YGERFPD 11
 :|||
 Db 2 HGSHTDEEF 11

RESULT 4
 TKN4_PSEGU STANDARD; PRT; 11 AA.
 ID TKN4_PSEGU
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide I (PG-SPI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.

Query Match 33.3%; Score 21; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri."
 RL Peptides 11:299-304(1990).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; E60409; E60409.
 DR InterPro; IPR002040; Tachy Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 11 11
 FT SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 33.3%; Score 21; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PDENF 11
 :|||
 Db 4 PDEFF 8

RESULT 5

FIF1_SARBU STANDARD; PRT; 12 AA.
 ID FIF1_SARBU
 AC P83349;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FIRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 RC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438685;
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
 RT "Identification in Drosophila melanogaster of the invertebrate G
 protein-coupled FMRamide receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
 CC junctions.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD RES 12 12
 FT MOD RES 12 12
 FT SEQUENCE 12 AA; 1389 MW; 2DC4519C14AB5A7 CRC64;

Query Match 33.3%; Score 21; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 5.6e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 PDENF 11
 :|||
 Db 5 PSDNF 9

```

RESULT 6
FAR2_MACRS
ID FAR2_MACRS STANDARD; PRT; 10 AA.
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP7 (GYGDRNPLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match
Best Local Similarity 31.7%; Score 20; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGER 5
DB 2 YGDR 5

RESULT 7
LPER_BACLI
ID LPER_BACLI STANDARD; PRT; 14 AA.
AC Q04303;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Erythromycin resistance leader peptide (23S rRNA methylase leader
DE peptide).
OS Bacillus licheniformis, and
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402, 1392;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.licheniformis;
RX MEDLINE=84245158; PubMed=6429477;
RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;
RT "DNA sequence and regulation of ermD, a macrolide-lincosamide-
RT streptogramin B resistance element from Bacillus licheniformis.";
RL Mol. Gen. Genet. 194:349-356(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.licheniformis; STRAIN=EMR-1;
RX MEDLINE=91310580; PubMed=1713206;
RA Kwak J.-K., Choi E.-C., Weisblum B.;
RT "Transcriptional attenuation control of ermK, a
RT macrolide-lincosamide-streptogramin B resistance determinant from
RT Bacillus licheniformis.";
RL J. Bacteriol. 173:4725-4735(1991).
RN [3]
RP SEQUENCE FROM N.A.

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RC SPECIES=B.anthraxis; STRAIN=590;
RX MEDLINE=93232776; PubMed=8473865;
RA Kim H.-S., Choi E.-C., Kim B.-K.;
RT "A macrolide-lincosamide-streptogramin B resistance determinant from
RT Bacillus anthracis 590: cloning and expression of ermJ.";
RL J. Gen. Microbiol. 139:601-607(1993).
CC -1- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF
CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B
CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08389; AAA22596.1; -.
DR EMBL; M29832; AAA22598.1; -.
DR PIR; A42473; A42473.
KW Antibiotic resistance; Leader peptide.
SQ SEQUENCE 14 AA; 1732 MW; 5D1338B59F32ED07 CRC64;

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Query Match
Best Local Similarity 31.7%; Score 20; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 5 RFPDEN 10
DB 8 RFPPLN 13

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RESULT 8
FAR2_MACRS
ID FAR2_MACRS STANDARD; PRT; 8 AA.
AC P83275;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP2 (ADKNFLRF-amide).
DE Macrobrachium rosenbergii (Giant fresh water prawn).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

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Query Match
Best Local Similarity 30.2%; Score 19; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 8 DENF 11
DB 2 DKNF 5

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RESULT 9
FAR3_MACRS

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ID FAR3 MACRS STANDARD; PRT; 9 AA.
AC P83276;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonidae; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433AB CRC64;

Query Match 30.2%; Score 19; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
DB 3 DXNF 6

RESULT 10
EFG_CLOPA STANDARD; PRT; 11 AA.
ID EFG_CLOPA
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrid R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro: IPR000795; EF_GTPbind.
DR PROSITE: PS00301; EFATOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412571F1D9C33B17 CRC64;

Query Match 30.2%; Score 19; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 RFPDENF 11
DB 1 KYPLEKF 7

RESULT 11
FAR1_PENMO STANDARD; PRT; 8 AA.
ID FAR1_PENMO
AC P8316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP1 (GDRNFLRF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaitrathangkur P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DENF 11
DB 2 DRNF 5

RESULT 12
FAR3_HOMAM STANDARD; PRT; 8 AA.
ID FAR3_HOMAM
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide 3 (Flt 3) (F2).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; PubMed=3429714;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRamide-like immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides.";
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 nm
CC potassium in the presence of calcium.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD_RES 8
```

SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match

Best Local Similarity 28.6%; Score 18; DB 1; Length 8;
Matches 3; Conservativity 75.0%; Pred. No. 1.4e+05; Mismatches 0; Indels 0; Gaps 0;

OY 8 DENF 11
| | |
Db 2 DRNF 5

RESULT 13

UPA3_HUMAN

ID UPA3_HUMAN STANDARD; PRT; 9 AA.

AC P30089;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RC TISSUE=Plasma;

RX MEDLINE=93092937; PubMed=1459097;

RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,

RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,

RA Hochstrasser D.F.;

RT "Plasma protein map: an update by microsequencing.";

RL Electrophoresis 13:707-714(1992).

CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown

CC protein is: 4.6, its MW is: 46 kDa.

DR SWISS-2DPAGE; P30089; HUMAN.

FT NON_TER 1

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FT NON_TER 1

Query Match
Best Local Similarity 28.6%; Score 18; DB 1; Length 9;
Matches 3; Conservativity 50.0%; Pred. No. 1.4e+05; Mismatches 2; Indels 0; Gaps 0;

OY 6 PDENF 11
| | |
Db 4 PXYTDF 9

RESULT 14

PNEU_RAT

ID PNEU_RAT STANDARD; PRT; 10 AA.

AC P21936;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pneumadin (PNM).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Lung;

RX MEDLINE=91110910; PubMed=2274681;

RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;

RA "Pneumadin: a new lung peptide which triggers antidiuresis.";

RL Regul. Pept. 30:77-87(1990).

CC -1- FUNCTION: This antidiuretic peptide triggers the release of ADH.

DR PIR; A33143; A33143.

KM Amidation.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match
Best Local Similarity 28.6%; Score 18; DB 1; Length 10;

Matches 3; Conservativity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4
| | |
Db 1 YGE 3

RESULT 15

RT02_BOVIN

ID RT02_BOVIN STANDARD; PRT; 10 AA.

AC P82923;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).

GN MRPS2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=21276436; PubMed=11279123;

RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;

RA "The small subunit of the mammalian mitochondrial ribosome:

RT identification of the full complement of ribosomal proteins present.";

RL J. Biol. Chem. 276:19363-19374(2001).

CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit

CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- SIMILARITY: Belongs to the S2P family of ribosomal proteins.

DR InterPro; IPR001865; Ribosomal_S2.

DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.

KW Ribosomal protein; Mitochondrion.

FT NON_TER 1

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Query Match
Best Local Similarity 28.6%; Score 18; DB 1; Length 10;

Matches 3; Conservativity 60.0%; Pred. No. 1.6e+03; Mismatches 1; Indels 0; Gaps 0;

OY 1 IYGER 5
| | |
Db 6 IFGSR 10

RESULT 16

TKN1_PSEGU

ID TKN1_PSEGU STANDARD; PRT; 11 AA.

AC P42986;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Kassinin-like peptide K-1 (PG-K1).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of

the Australian frog Pseudophryne guentheri.";

peptides 11:299-304(1990).

```
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR: B60409; B60409.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR InterPro: IPR008215; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CBA1B7 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDE 9
DB 4 PDE 6

RESULT 17
TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Endean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR InterPro: IPR008215; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDP457 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDE 10
DB 4 PDE 6
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DB 2 PDPN 5

RESULT 18
TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR: C60409; C60409.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR InterPro: IPR008215; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CBA1B7 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDE 9
DB 4 PDE 6

RESULT 19
PSP3_PHYPA STANDARD; PRT; 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (24 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
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RL  Planta 201:261-272(1997).
CC  -1- FUNCTION: May be involved in the regulation of photosystem II.
CC  -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC  with the photosystem II complex.
CC  -1- INDUCTION: By light.
CC  -1- SIMILARITY: Belongs to the psbp family.
KW  Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
KW  Multigene family.
FT  NON TER 12
SQ  SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGE 4
DB 2 YGE 4

RESULT 20
NP3_LYMST STANDARD; PRT; 13 AA.
ID NP3_LYMST
AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 3.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "Lymnaea stagnalis. A new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32473; S32473.
KW Neuropeptide; Amidation.
FT MOD_RES 13
FT UNSURE 12
SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 IYGERFPD 8
DB 5 ISGSAFSD 12

RESULT 21
PSBP_PINPS STANDARD; PRT; 13 AA.
ID PSBP_PINPS
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
GN PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.

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RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahrmann N., Kremer A.,
RA Frigerio J.-M., Plomieu C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: May be involved in the regulation of photosystem II.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N179) is: 5.9, its MW is: 22 kDa.
CC -1- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON TER 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 28.6%; Score 18; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGE 4
DB 2 YGE 4

RESULT 22
MARI_ALTSP STANDARD; PRT; 14 AA.
ID MARI_ALTSP
AC P29399;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinstatin C-2 [Marinostatin C-1; Marinostatin D].
OS Alteromonas sp. (strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamei K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31.";
RL J. Biochem. 110:856-858(1991).
CC -1- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14 MARINOSTATIN C-2.
FT PEPTIDE 3 14 MARINOSTATIN C-1.
FT PEPTIDE 4 14 MARINOSTATIN D.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 6 7 REACTIVE BOND.
SQ SEQUENCE 14 AA; 1644 MW; 6E7CEFP92EF32E44 CRC64;

Query Match 28.6%; Score 18; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPDEN 10
DB 7 RYPSDD 12

RESULT 23
FARI_PANRE STANDARD; PRT; 8 AA.
ID FARI_PANRE
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PFI (SDPNFLRF-amide).
OS Panagrellus redivivus.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RT "Two FMRamide-like peptides from the free-living nematode
Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -1- FUNCTION: Myoactive.
CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located
caudally to the base of the pharynx.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DENE 11
Db 2 DPNF 5

RESULT 24

PAR2_PANRE STANDARD; PRT; 9 AA.
ID FAR2_PANRE
AC P41873;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide PF2 (SADPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RT "Two FMRamide-like peptides from the free-living nematode
Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -1- FUNCTION: Myoactive.
CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located
caudally to the base of the pharynx.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 27.0%; Score 17; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DENE 11
Db 3 DPNF 6

RESULT 25

FAR4_CALVO STANDARD; PRT; 9 AA.
ID FAR4_CALVO
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RT Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; D41978; D41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDENE 11
Db 2 PNQDF 6

RESULT 26

UPA8_HUMAN STANDARD; PRT; 10 AA.
ID UPA8_HUMAN
AC P30094;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 7.2, its MW is: 16 kDa.
DR SWISS-2DPAGE; P30094; HUMAN.
FT NON_TER 1
FT VARIANT 4
FT NON_TER 4
FT NON_TER 4
SQ SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IYGERFP 7
Db 1 IVGSKXP 7

RESULT 27

LSK1_LEUMA
ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -1- FUNCTION: Change the frequency and amplitude of contractions of
the hindgut. Inhibits muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 27.0%; Score 17; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
|:|
|:|
Db 1 EQFED 5

RESULT 28
LSKP_PERAM
ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CKK-like neuropeptides from
the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -1- FUNCTION: Stimulates hindgut contractions.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAB CRC64;

Query Match 27.0%; Score 17; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
|:|
|:|
Db 1 EQFED 5

RESULT 29
ADFB_TENMO
ID ADFB_TENMO STANDARD; PRT; 13 AA.
AC P83109;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor B (ADFB).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=22465067; PubMed=12576082;
RA Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
RA Hull J.J., Schooley D.A.;
RT "Isolation, identification and localization of a second beetle
antidiuretic peptide.";
RL Peptides 24:27-34(2003).
CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
cGMP as second messenger. May function as an antidiuretic
hormone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
pairs of bilaterally symmetrical cells in the protocerebrum.
CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
KW Neuropeptide; Hormone.
SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;

Query Match 27.0%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3
|:|
|:|
Db 10 IYG 12

RESULT 30
NSK2_SARBU
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Neosulfakinin-II (NEB-SK-II).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: Myotropic peptide.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A56632; A56632.
DR InterPro; IPR001651; Gastrin.

DR PROSITE: PS00259; GASTRIN; 1.
 KW Neuropetide; Amidation; Sulfation.
 FT MOD_RES 9 9 SULFATION (POTENTIAL).
 FT MOD_RES 14 14 AMIDATION (POTENTIAL).
 SQ SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;

Query Match
 Best Local Similarity 27.0%; Score 17; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPD 8
 DB 4 EQFDD 8

RESULT 31

TKN1_SCHGR STANDARD; PRT; 14 AA.

AC P82470;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tachykinin-1 (Scg-midgut-TK).
 OS Schistocerca gregaria (Desert locust).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 CC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
 OX NCBI_Taxid=7010;

RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Midgut;
 RX MEDLINE=20050081; PubMed=10581195;
 RA Veelaert D., Baggerman G., Derva R., Maelkens E., Meusen T.,
 RA Vande Water G., De loof A., Schoofs L.;
 RT "Identification of a new tachykinin from the midgut of the desert
 locust, Schistocerca gregaria, by ESI-Qq-TOF mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 266:237-242(1999).
 CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
 of spontaneous contractions and tonus of hindgut muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Midgut.
 CC -1- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray.
 CC -1- SIMILARITY: SIMILAR TO THE COCKROACH LENTRP 3, A TACHYKININ-
 RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.

KW Tachykinin; Neuropetide; Amidation.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1496 MW; CA4C578C0169FC72 CRC64;

Query Match
 Best Local Similarity 27.0%; Score 17; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGER 5
 DB 11 YGTR 14

RESULT 32

UC04_MAIZE STANDARD; PRT; 14 AA.

AC P80610;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 128)
 DE (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_Taxid=4577;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerwal C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program";
 RT Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 protein is: 6.8, its MW is: 34.6 kDa.
 DR Maize-2DPAGE; P80610; COLEOPTILE.
 FT MOD_RES 14 14
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1393 MW; C14451BA1116D4AD CRC64;

Query Match
 Best Local Similarity 27.0%; Score 17; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DENF 11
 DB 2 DEGF 5

RESULT 33

ALL1_CYPPO STANDARD; PRT; 8 AA.

AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydia pomonella (Codling moth).
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_Taxid=82600;

RN [1]
 RP SEQUENCE.

RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duvé H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 CC Neuropetide; Amidation.

KW Neuropetide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match
 Best Local Similarity 25.4%; Score 16; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 PDENF 11
 DB 2 PHYNF 6

RESULT 34

FA7_ASCSU STANDARD; PRT; 8 AA.

AC P43171;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropetide AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 CC Ascarididae; Ascaris.
 OX NCBI_Taxid=6253;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=95380362; PubMed=7651904;

RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 8 AA; 963 MW; 9CD40059D417687D CRC64;
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 25.4%; Score 16; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERP 6
Db 2 GPRF 5

RESULT 35

FAR1_CALVO STANDARD; PRT; 9 AA.
ID FAR1_CALVO
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR: A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11
Db 2 PQQDF 6

RESULT 36

FAR2_CALVO STANDARD; PRT; 9 AA.
ID FAR2_CALVO
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;

RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR: B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11
Db 2 PQQDF 6

RESULT 37

FAR3_CALVO STANDARD; PRT; 9 AA.
ID FAR3_CALVO
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
CC salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR: C41978; C41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11
Db 2 PQQDF 6

RESULT 38

FRF1_SARBU STANDARD; PRT; 9 AA.
ID FRF1_SARBU
AC P83350;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11
DB 2 PSQDF 6

RESULT 39
TKC1 CALVO STANDARD; PRT; 9 AA.
ID TKC1 CALVO
AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clotens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -1- FUNCTION: Myoactive peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CD1B7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5
DB 6 YGVR 9
```

```
RESULT 40
TKC1 LOCMI STANDARD; PRT; 9 AA.
ID TKC1 LOCMI
AC P16223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the
CC oviduct and foregut.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; S08265; ECLQIM.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C85A7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5
DB 6 YGVR 9

RESULT 41
PORB_METT STANDARD; PRT; 10 AA.
ID PORB_METT
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyruvate synthase subunit porb (EC 1.2.7.1) (Pyruvate oxidoreductase
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
DE (Fragment).
DE PORB.
GN Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OS Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Teeseegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -1- CATALYTIC ACTIVITY: Pyruvate + COA + oxidized ferredoxin = acetyl-
CC COA + CO(2) + reduced ferredoxin.
CC -1- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC gamma chain.
CC -1- MISCELLANEOUS: Has a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;
```

Query Match 25.4%; Score 16; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.8e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11
 DB 4 PEQXF 8

RESULT 42

PPCK_FASHE STANDARD; PRT; 10 AA.
 AC P80525;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
 DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile
 DE protein 1) (Fragment).
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9536693; PubMed=7639732;
 RA Tkalcovic J., Ashman K., Meusen E.;
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile
 RT proteins.";
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
 CC + CO(2).
 CC -1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxykinase [GTP]
 CC family.
 CC Interpro; IPR008209; PEP carboxykin.
 DR PROSITE; PS00505; PEPCK_GTP; PARTIAL.
 KW Lyase; Decarboxylase; GTP-binding.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPD 8
 DB 1 YPD 3

RESULT 43

TKL2_LOCM1 STANDARD; PRT; 10 AA.
 AC P16224;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Locustatachykinin II (TK-II).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the
 CC oviduct and foregut.
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.

DR PIR; S08266; ECLQ2M.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5
 DB 7 YGVR 10

RESULT 44

TKL3_LOCM1 STANDARD; PRT; 10 AA.
 AC P30249;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Locustatachykinin III (TK-III).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=91219696; PubMed=2132575;
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
 RA de Loof A.;
 RT "Locustatachykinin III and IV: two additional insect neuropeptides
 RT with homology to peptides of the vertebrate tachykinin family.";
 RL Regul. Pept. 31:199-212(1990).
 CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the
 CC oviduct and foregut.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 DR PIR; A60073; ECLQ3M.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGER 5
 DB 7 YGVR 10

RESULT 45

TKS1_AEDAE STANDARD; PRT; 10 AA.
 AC P42634;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sialokinin I.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Rockefeller; TISSUE=salivary gland;
 RX MEDLINE=94105119; PubMed=8278354;
 RA Champagne D.E., Ribeiro J.M.C.;

RA "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
 CC oviduct and foregut.
 CC -1- SUBCELLULAR LOCATION: Secreted.

RT mosquito Aedes aegypti.
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
 CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the
 CC site of feeding.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A49581; A49581.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1145 MW; 3DCFDE6B59C33AA8 CRC64;

Query Match 25.4%; Score 16; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERF 6
 Db 3 GDKF 6

Search completed: August 30, 2004, 10:50:22
 Job time : 2.89527 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.30743 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-6
Perfect score: 63
Sequence: 1 IYGERFPDENF 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	39.7	10	2	A60476	S-layer protein -
2	24	38.1	9	2	PT0315	Ig heavy chain CRD
3	23	36.5	12	2	S26556	T-cell receptor be
4	23	36.5	12	2	PA00047	protein QA100045 -
5	21	33.3	11	2	E60409	substance P-like p
6	20	31.7	9	2	PT0324	Ig heavy chain CRD
7	20	31.7	13	2	S29488	GTP-binding protei
8	20	31.7	14	2	A42473	ermK leader peptid
9	19	30.2	8	2	A46306	spasmogenic toxin
10	19	30.2	10	2	B56899	serum heterodimer,
11	19	30.2	12	2	S26554	T-cell receptor be
12	19	30.2	13	2	S47362	T-cell antigen rec
13	18	28.6	8	2	PH1407	Ig heavy chain V r
14	18	28.6	9	2	S10784	enamelin i - bovin
15	18	28.6	10	2	B33710	ornithine decarbox
16	18	28.6	10	2	A33143	pneumadin - rat
17	18	28.6	11	2	B60409	kassinin-like pept
18	18	28.6	11	2	C60409	kassinin-like pept
19	18	28.6	11	2	S07203	uperolein - frog (
20	18	28.6	12	2	S26552	T-cell receptor be
21	18	28.6	12	2	PQ0730	unidentified 5.4/3
22	18	28.6	13	2	S32473	lymadFamide 3 - 9
23	18	28.6	14	2	G44957	photosystem II oxy
24	18	28.6	14	2	A54370	inorganic diphosph
25	17	27.0	9	2	G58502	kidney and bladder
26	17	27.0	9	2	D41978	calliferramide 4 -
27	17	27.0	9	2	S36850	Ig heavy chain V r
28	17	27.0	9	2	I49406	bone gla protein -
29	17	27.0	10	2	PQ0753	beta-fructofuranos

30	17	27.0	10	2	A61354	carnitine medium/1
31	17	27.0	11	1	GMROL	leucosulfakinin -
32	17	27.0	11	2	A58502	38K kidney stone p
33	17	27.0	11	2	UQ2307	hypothetical 1.5K
34	17	27.0	11	2	A60656	perisulfakinin - A
35	17	27.0	11	2	S23926	major glycoprotein
36	17	27.0	12	2	PH1462	T-cell receptor be
37	17	27.0	13	2	A32734	nekephalin precurs
38	17	27.0	14	2	A56632	neosulfakinin-II -
39	17	27.0	14	2	PH1356	Ig heavy chain DJ
40	17	27.0	14	2	A59018	MUCl enhancer bind
41	16.5	26.2	12	2	S15815	translation elonga
42	16	25.4	8	2	S11078	glucose-6-phosphat
43	16	25.4	8	2	PT0653	T-cell receptor be
44	16	25.4	9	2	A61230	calsequestrin, car
45	16	25.4	9	2	D57444	neuropeptide Grb-A

ALIGNMENTS

RESULT 1
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C/Species: Bacillus thuringiensis
C/Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
C/Accession: A60476
R/Luckevich, M.D.; Beveridge, T.U.
J. Bacteriol. 171, 6656-6667, 1989
A/Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A/Reference number: A60476; MUID:90078111; PMID:2592346
A/Accession: A60476
A/Molecule type: protein
A/Residues: 1-10 <LUC>
C/Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 39.7%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GERFPD 8
Db 2 GKTFPD 7

RESULT 2
PT0315
Ig heavy chain CRD3 region (clone 6-109) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0315
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0315
A/Molecule type: DNA
A/Residues: 1-9 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GERFPDENF 11
Db 1 GERFLSF 9

RESULT 3
S26556
T-cell receptor beta chain (clone Cw3/2C3) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26556
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26556
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X68006
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/2C3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 36.5%; Score 23; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGER 5
|||
Db 5 YGER 8

RESULT 4

PA0047
Protein QA100045 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0047
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A;Reference number: PA0001
A;Accession: PA0047
A;Molecule type: protein
A;Residues: 1-12 <KAM>

Query Match 36.5%; Score 23; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERPD 8
|||
Db 5 GDXLPD 10

RESULT 5

E60409
Substance P-like peptide I - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C;Accession: E60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: E60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 33.3%; Score 21; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PDENF 11
|||
Db 4 PDFFF 8

RESULT 6

PT0324
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0324
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 31.7%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERF 6
|||
Db 4 YGESY 8

RESULT 7

S29488
GTP-binding protein o-rab3 - marbled electric ray (fragment)
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S29488
R;Volkmann, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A;Reference number: S29485; MUID:93154521; PMID:8428634
A;Accession: S29488
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <VOL>

Query Match 31.7%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DENF 11
|||
Db 5 DQNF 8

RESULT 8

A42473
ermK leader peptide - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Sep-1999
C;Accession: A42473; I39884
R;Kwak, J.H.; Choi, E.C.; Weisblum, B.
J. Bacteriol. 173, 4725-4735, 1991
A;Title: Transcriptional attenuation control of ermK, a macrolide-lincosamide-streptogram
A;Reference number: A42473; MUID:91310580; PMID:1713206
A;Accession: A42473
A;Molecule type: DNA
A;Residues: 1-14 <KWA>
R;Gryczan, T.; Israeli-Reches, M.; Del Bue, M.; Dubnau, D.A.
Mol. Gen. Genet. 194, 349-356, 1984
A;Title: DNA sequence and regulation of ermD, a macrolide-lincosamide-streptogramin B res
A;Reference number: I39884; MUID:84245158; PMID:6429477
A;Accession: I39884
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-14 <RES>
A;Cross-references: GB:M29832; NID:G143199; PIDN:AAA22598.1; PID:G143200
C;Superfamily: unassigned leader peptides

Query Match 31.7%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 RFPDEN 10
|||
Db 8 RFPDEN 13

RESULT 9

A46306
spasmogenic toxin PNV1 - spider (Phoneutria nigriventer) (fragment)
C/Species: Phoneutria nigriventer
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C/Accession: A46306
R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicol 31, 377-384, 1993
A/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A/Reference number: A46306; MUID:93276438; PMID:8503129
A/Accession: A46306
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <MAR>

Query Match 30.2%; Score 19; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 ERFPDEN 10
|||
Db 1 EAFPGQS 7

RESULT 10

B56899
serum heterodimer, 24K chain - sandbar shark (fragment)
C/Species: Carcharhinus plumbeus (sandbar shark)
C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C/Accession: B56899
R/Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
Comp. Biochem. Physiol. B 103, 563-568, 1992
A/Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum by
A/Reference number: A56899; MUID:93092592; PMID:1458832
A/Accession: B56899
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <VAZ>
C/Keywords: glycoprotein; plasma

Query Match 30.2%; Score 19; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFPE 9
|||
Db 4 GERVYNE 10

RESULT 11

S26534
T-cell receptor beta chain (clone Cw3/Cas7) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C/Accession: S26534
R/Casanova, J.L.; Cerottini, J.C.; Matches, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: S26534
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X68004

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas7
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 30.2%; Score 19; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGER 5
|||
Db 5 YGER 8

RESULT 12

S47362
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47362
R/Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A/Reference number: S47355
A/Accession: S47362
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35688; NID:9527465; PIDN:CAA84757.1; PID:9527466
C/Keywords: T-cell receptor

Query Match 30.2%; Score 19; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERF 6
|||
Db 8 YNEQF 12

RESULT 13

PH1407
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C/Accession: PH1407
R/Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tai
J. Exp. Med. 176, 1209-1214, 1992
A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t
la virus.
A/Reference number: PH1403; MUID:93018837; PMID:1402663
A/Accession: PH1407
A/Molecule type: DNA
A/Residues: 1-8 <SHI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFP 7
|||
Db 6 RFP 8

RESULT 14

S10784
enamelin i - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
R/Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990

A/Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A/Reference number: S10780; MUID:90336641; PMID:2379503
A/Accession: S10784
A/Molecule type: protein
A/Residues: 1-9 <STR>
C/Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 EPDENE 11
DB 1 FPYDGF 6

RESULT 15
B33710
ornithine decarboxylase leader peptide - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 24-Sep-1999
C/Accession: B33710

R/Wen, L.; Huang, J.K.; Blackshear, P.J.

J. Biol. Chem. 264, 9016-9021, 1989

A/Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory ele

A/Reference number: A33710; MUID:89255378; PMID:2722815

A/Accession: B33710

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: mRNA

A/Residues: 1-10 <WEN>

A/Cross-references: GB:J04791; NID:9205807; PIDN:AAA6163.1; PID:9806309

C/Superfamily: unassigned leader peptides

Query Match 28.6%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFP 7
DB 6 RFP 8

RESULT 16
A33143

pneumadin - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 18-Aug-2000

C/Accession: A33143

R/Batra, V.K.; Mathur, M.; Mir, S.A.; Kapoor, R.; Kumar, M.A.

Regul. Pept. 30, 77-87, 1990

A/Title: Pneumadin: a new lung peptide which triggers antidiuresis.

A/Reference number: A33143; MUID:91110910; PMID:2274681

A/Accession: A33143

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <BAT>

C/Superfamily: unassigned animal peptides

Query Match 28.6%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4
DB 1 YGE 3

RESULT 17
B60409

kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C/Species: Pseudophryne guentheri

C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C/Accession: B60409

R/Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990

A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral

A/Reference number: A60409; MUID:90287814; PMID:2356157

A/Accession: B60409

A/Molecule type: protein

A/Residues: 1-11 <SIM>

A/Note: this peptide was also found in a deamidated form

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/1/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 28.6%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9
DB 4 PDE 6

RESULT 18
C60409

kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C/Species: Pseudophryne guentheri

C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C/Accession: C60409

R/Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral

A/Reference number: A60409; MUID:90287814; PMID:2356157

A/Accession: C60409

A/Molecule type: protein

A/Residues: 1-11 <SIM>

A/Note: this peptide was also found in a deamidated form

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/1/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 28.6%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9
DB 4 PDE 6

RESULT 19
S07203

uperolein - frog (Uperoleia marmorata)

C/Species: Uperoleia marmorata

C/Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C/Accession: S07203

R/Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975

A/Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin

A/Reference number: S07203; MUID:75131227; PMID:1120493

A/Accession: S07203

A/Molecule type: protein

A/Residues: 1-11 <ANA>

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 28.6%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 PDEN 10

Db 2 PDPN 5

RESULT 20

S26552
T-cell receptor beta chain (clone Cw3/701.1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C/Accession: S26552
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: S26552
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X68002
A/Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 28.6%; Score 18; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4
|||
Db 5 YGE 7

RESULT 21

PQ0730
unidentified 5.4/35K protein [imported] - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C/Accession: PQ0730
R/Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A/Reference number: PQ0696
A/Accession: PQ0730
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <KOM>

Query Match 28.6%; Score 18; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4
|||
Db 8 YGE 10

RESULT 22

S32473
LymnadFamide 3 - great pond snail
C/Species: Lymnaea stagnalis (great pond snail)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C/Accession: S32473
R/Johnsen, A.H.; Rehfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A/Title: LymnadFamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis
A/Reference number: S32471; MUID:93238777; PMID:8477756
A/Accession: S32473
A/Molecule type: protein
A/Residues: 1-13 <JOH>
A/Cross-references: PIDN:AAB26364.1; PID:G299831
A/Experimental source: ganglia
C/Keywords: amidated carboxyl end; neuropeptide
F,13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 18; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 IYGERFPD 8
|||
Db 5 ISGSAFSD 12

RESULT 23

G44957
photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsun NN) (fragment)
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993
C/Accession: G44957
R/Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
Plant Cell Physiol. 31, 215-221, 1990
A/Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum
A/Reference number: A44957
A/Accession: G44957
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <TAK>

Query Match 28.6%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGE 4
|||
Db 2 YGE 4

RESULT 24

A54370
inorganic diphosphatase (EC 3.6.1.1) - cucurbit (fragment)
C/Species: Cucurbita sp. (cucurbit)
C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 03-Jun-2002
C/Accession: A54370
R/Sato, M.H.; Kasahara, M.; Ishii, N.; Homareda, H.; Matsui, H.; Yoshida, M.
J. Biol. Chem. 269, 6725-6728, 1994
A/Title: Purified vacuolar inorganic pyrophosphatase consisting of a 75-kDa polypeptide
A/Reference number: A54370; MUID:94165068; PMID:8120031
A/Accession: A54370
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <SAT>
C/Keywords: hydrolase

Query Match 28.6%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDE 9
|||
Db 11 PDE 13

RESULT 25

G58502
kidney and bladder stone protein - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C/Accession: G58502
R/Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.
A/Reference number: A58501
A/Accession: G58502
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <BIN>
A/Experimental source: human kidney stone, bladder stone

A>Note: a secondary sequence AAKENPXD was also found

Query Match 27.0%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PDENF 11
Db 3 PDVXF 7

RESULT 26

D41978
callifmrfamide 4 - bluebottle fly (Calliphora vomitoria)

C/Species: Calliphora vomitoria

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

C/Accession: D41978

R/Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi

A/Reference number: A41978; MUID:92196111; PMID:1549595

A/Accession: D41978

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <DUV>

C/Keywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDENF 11
Db 2 PNQDF 6

RESULT 27

S36850

IG heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

C/Accession: S36850

R/Jacob, J.; Kelsoe, G.

submitted to the EMBL Data Library, July 1992

A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny

A/Reference number: S25024

A/Accession: S36850

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-9 <JAC>

A/Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799.1; PID:es1594; PID:g1333871
C/Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERF 6
Db 5 YGSYF 9

RESULT 28

I49406

bone gla protein - western wild mouse (fragment)

C/Species: Mus spretus (western wild mouse)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C/Accession: I49406

R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A/Reference number: I48934; MUID:94319082; PMID:8043949

A/Accession: I49406
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-9 <RES>
A/Cross-references: EMBL:U05695; NID:g497015; PIDN:AAB60465.1; PID:g642828

Query Match 27.0%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYG 3
Db 4 IYG 6

RESULT 29

PQ0753

beta-fructofuranosidase (EC 3.2.1.26) IIB - barley (fragment)

C/Species: Hordeum vulgare (barley)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 23-Mar-1995

C/Accession: PQ0753

R/Oberland, D.M.; Simmen, U.; Boller, T.; Wiemken, A.

Plant Physiol. 101, 1331-1339, 1993

A/Title: Purification and characterization of three soluble invertases from barley (Horde

A/Reference number: PQ0752; MUID:94143483; PMID:8310063

A/Accession: PQ0753

A/Molecule type: protein

A/Residues: 1-10 <OBE>

A/Experimental source: leaf, cv. Express

C/Keywords: alternative initiators; glycoprotein; glycosidase; hydrolase

Query Match 27.0%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PPDEN 10
Db 2 PPWDN 6

RESULT 30

A61354

carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)

N/Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRP58;

C/Species: Rattus norvegicus (Norway rat)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C/Accession: A61354

R/Murthy, M.S.R.; Pande, S.V.

Mol. Cell. Biochem. 122, 133-138, 1993

A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previc

A/Reference number: A61354; MUID:94049728; PMID:8232244

A/Accession: A61354

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <MUR>

C/Keywords: acyltransferase

Query Match 27.0%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DEN 10
Db 8 DEN 10

RESULT 31

GMROL

leucosulfakinin - Madeira cockroach

N/Alternate names: LSK

C/Species: Leucophaea maderae (Madeira cockroach)

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C/Accession: A01622

R,Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A/Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch

A/Reference number: A01622; MUID:86315858; PMID:3749893

A/Accession: A01622

A/Molecule type: protein

A/Residues: 1-11 <NAC>

A/Superfamily: gastrin

C/Keywords: amidated carboxyl end; hormone; sulfoprotein

F/6/Binding site: sulfate (Tyr) (covalent) #status experimental

F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 1; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8

Db 1 EQFED 5

RESULT 32

A58502 38K kidney stone protein - unidentified bacterium (fragment)

C/Species: unidentified bacterium

C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C/Accession: A58502

R/Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: A58501

A/Accession: A58502

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-11 <BIN>

A/Experimental source: human kidney stone containing Ca ox.mono and dihyd, 1% struvite,

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFP 7

Db 7 GAXFP 11

RESULT 33

JQ2307 hypothetical 1.5K protein - tomato chloroplast (strain Toko)

C/Species: chloroplast Lycopersicon esculentum (tomato)

C/Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 23-Mar-1995

C/Accession: JQ2307

R/Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A/Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A/Reference number: JQ2306

A/Accession: JQ2307

A/Molecule type: DNA

A/Residues: 1-11 <KAW>

A/Experimental source: strain Toko

C/Genetics:

A/Genome: chloroplast

C/Keywords: chloroplast

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERF 6

Db 4 YDEEF 8

RESULT 34

A60656

perisulfakinin - American cockroach

C/Species: Periplaneta americana (American cockroach)

C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 11-Jul-1997

C/Accession: A60656

R/Veenstra, J.A.

Neuropeptides 14, 145-149, 1989

A/Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American

A/Reference number: A60656; MUID:90137190; PMID:2615921

A/Accession: A60656

A/Molecule type: protein

A/Residues: 1-11 <VEE>

C/Comment: This neuropeptide stimulates hindgut contractions.

C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F/6/Binding site: sulfate (Tyr) (covalent) #status experimental

F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8

Db 1 EQFDD 5

RESULT 35

S23926

major glycoprotein PAS-6 - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999

C/Accession: S23926

R/Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992

A/Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from

A/Reference number: S23926; MUID:92353107; PMID:1643094

A/Accession: S23926

A/Molecule type: protein

A/Residues: 1-11 <KIM>

C/Keywords: glycoprotein; milk; blocked amino end

Query Match 27.0%; Score 17; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 5.1e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GERPDE 9

Db 3 GNKPSE 9

RESULT 36

PH1462

T-cell receptor beta chain (clone A24/PEF1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995

C/Accession: PH1462

R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko

J. Exp. Med. 177, 811-820, 1993

A/Title: T cell receptor selection by and recognition of two class I major histocompatib

A/Reference number: PH1430; MUID:93171821; PMID:8436911

A/Accession: PH1462

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

A/Experimental source: cytolytic T-lymphocyte

C/Superfamily: immunoglobulin homology

C/Keywords: receptor; T-cell

Query Match 27.0%; Score 17; DB 2; Length 12;

Best Local Similarity 60.0%; Pred. No. 5.6e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PDENF 11

Db 7 PDYTF 11

RESULT 37

A32734
enkephalin precursor - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000
C/Accession: A32734
R/Micanovic, R.; Ray, P.; Kruggel, W.; Lewis, R.V.
Biochem. Biophys. Res. Commun. 118, 299-303, 1984
A/Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin
A/Reference number: A32734; MUID:84128045; PMID:5546517
A/Accession: A32734
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <MTC>
C/Superfamily: proenkephalin
C/Keywords: neuropeptide; opioid peptide

Query Match 27.0%; Score 17; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.1e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 IYGRF 6
: : :
Db 4 VLGRY 9

RESULT 38

A56632
neosulfakinin-II - flesh fly (Sarcophaga bullata)
N/Alternate names: Neb-SK-II
N/Contains: neosulfakinin-I (Neb-SK-I)
C/Species: Sarcophaga bullata
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C/Accession: A56632
R/Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.
Comp. Biochem. Physiol. C 103, 135-142, 1992
A/Title: Isolation and primary structure of two sulfakinin-like peptides from the flesh fly
A/Reference number: A56632; MUID:93083101; PMID:1360367
A/Accession: A56632
A/Molecule type: protein
A/Residues: 1-14 <FON>
A/Experimental source: heads
A/Note: sequence extracted from NCBI backbone (NCBI:120391)
C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F/1-14/Product: neosulfakinin-II #status experimental <NSK2>
F/6-14/Product: neosulfakinin-I #status experimental <NSK1>
F/9/Binding site: sulfate (Tyr) (covalent) #status predicted
F/14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPD 8
: : :
Db 4 EQFPD 8

RESULT 39

PH1356
Ig heavy chain DJ region (clone C178-97) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1356
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1356

A/Molecule type: DNA
A/Residues: 1-14 <WAS>
C/Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYG 3
: : :
Db 4 IYG 6

RESULT 40

A59018
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
R/Abbe, M.; Smith, C.J.; Larson, C.J.
Submitted to the Protein Sequence Database, May 1998
A/Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a breast cancer cell line MCF-7
A/Reference number: A59018
A/Accession: A59018
A/Molecule type: protein
A/Residues: 1-14 <ABB>
A/Experimental source: breast cancer cell line MCF-7
A/Note: 3-Val was also found
C/Keywords: DNA binding; heterodimer

Query Match 27.0%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYG 3
: : :
Db 4 IYG 6

RESULT 41

S15815
translational elongation factor eEF-2 - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 18-Mar-1997
C/Accession: S15815; S12970
R/Price, N.T.; Redbach, N.T.; Severinov, K.V.; Campbell, D.G.; Russell, J.M.; Proud, C.G.
FEBS Lett. 282, 253-258, 1991
A/Title: Identification of the phosphorylation sites in elongation factor-2 from rabbit
A/Reference number: S15815; MUID:91243806; PMID:2037042
A/Accession: S15815
A/Molecule type: protein
A/Residues: 1-12 <JMP>
R/Ovchinnikov, L.P.; Motuz, L.P.; Natapov, P.G.; Averbuch, L.J.; Wettenhall, R.E.H.; Seydov, F.B.S.
FEBS Lett. 275, 209-212, 1990
A/Title: Three phosphorylation sites in elongation factor 2.
A/Reference number: S12970; MUID:91085562; PMID:2261989
A/Accession: S12970
A/Molecule type: protein
A/Residues: 2-12 <OVC>
C/Superfamily: translational elongation factor 2; translation elongation factor Tu homology
C/Keywords: GTP binding; phosphoprotein; protein biosynthesis
F/8,10/Binding site: phosphate (Thr) (covalent) (by elongation factor 2 kinase) #status experimental

Query Match 26.2%; Score 16.5; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 3 GE-RFPD 8
: : :
Db 3 GERTFTD 9

RESULT 42

S11078

Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (*Pichia jadinii*) (fragment)
C/Species: *Pichia jadinii*, *Candida utilis*
C/Date: 30-Jun-1991 #sequence_revision 30-Sep-1991 #text_change 05-Aug-1994
C/Accession: S11078
R/Egestad, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Hol
FEBS Lett. 269, 194-196, 1990
A/Title: Fast atom bombardment mass spectrometry and chemical analysis in determinations
A/Reference number: S11074; MUID:90353571; PMID:2387402
A/Accession: S11078
A/Molecule type: protein
A/Residues: 1-8 <EGE>
A/Note: the source is designated as *Pichia jadinii*
C/Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway
F/1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 25.4%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGER 5
|||
Db 5 FGDR 8

RESULT 43

PT0653
T-cell receptor beta chain V-D-J region (121-3H) - mouse (fragment)
C/Species: *Mus musculus* (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0653
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:9127601; PMID:1711558
A/Accession: PT0653
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-8 <FEE>
A/Experimental source: day 4 postnatal thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match 25.4%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GER 5
|||
Db 6 GER 8

RESULT 44

A61230
calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)
N/Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-
C/Species: *Rana pipiens* (northern leopard frog)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C/Accession: A61230
R/Mcleod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A/Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular
rdium.
A/Reference number: A61230; MUID:91316784; PMID:1860177
A/Accession: A61230
A/Molecule type: protein
A/Residues: 1-9 <MCL>
C/Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei
C/Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c
C/Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi
C/Superfamily: calsequestrin
C/Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match

25.4%; Score 16; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFP 7
|||
Db 3 GLNFP 7

RESULT 45

D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C/Species: *Gryllus bimaculatus* (two-spotted cricket)
C/Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C/Accession: D57444
R/Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A/Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cric
A/Reference number: A57444; MUID:95403341; PMID:7673141
A/Accession: D57444
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <LOR>

Query Match 25.4%; Score 16; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERF 6
|||
Db 3 ERF 5

Search completed: August 30, 2004, 10:58:51
Job time : 4.30743 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 13.4527 Seconds

(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-6
Perfect score: 63
Sequence: 1 IYGERFPDENF 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues 149443
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29	46.0	10	14	US-10-194-441A-7	Sequence 7, Appl1
2	28	44.4	8	14	US-10-226-629A-477	Sequence 477, App
3	28	44.4	9	12	US-09-988-493-293	Sequence 293, App
4	28	44.4	9	12	US-10-014-340-209	Sequence 209, App
5	28	44.4	9	14	US-10-226-629A-478	Sequence 478, App
6	28	44.4	9	14	US-10-226-629A-491	Sequence 491, App
7	28	44.4	9	16	US-10-264-309-118	Sequence 118, App
8	28	44.4	10	14	US-10-226-629A-479	Sequence 479, App
9	28	44.4	10	14	US-10-226-629A-492	Sequence 492, App
10	28	44.4	10	14	US-10-226-629A-505	Sequence 505, App
11	28	44.4	11	14	US-10-226-629A-480	Sequence 480, App
12	28	44.4	11	14	US-10-226-629A-493	Sequence 493, App
13	28	44.4	11	14	US-10-226-629A-506	Sequence 506, App
14	28	44.4	11	14	US-10-226-629A-518	Sequence 518, App
15	28	44.4	12	14	US-10-286-457-432	Sequence 432, App

16	28	44.4	12	14	US-10-226-629A-481	Sequence 481, App
17	28	44.4	12	14	US-10-226-629A-494	Sequence 494, App
18	28	44.4	12	14	US-10-226-629A-507	Sequence 507, App
19	28	44.4	12	14	US-10-226-629A-519	Sequence 519, App
20	28	44.4	12	14	US-10-226-629A-530	Sequence 530, App
21	28	44.4	13	14	US-10-226-629A-482	Sequence 482, App
22	28	44.4	13	14	US-10-226-629A-495	Sequence 495, App
23	28	44.4	13	14	US-10-226-629A-508	Sequence 508, App
24	28	44.4	13	14	US-10-226-629A-520	Sequence 520, App
25	28	44.4	13	14	US-10-226-629A-531	Sequence 531, App
26	28	44.4	13	14	US-10-226-629A-541	Sequence 541, App
27	28	44.4	14	14	US-10-226-629A-483	Sequence 483, App
28	28	44.4	14	14	US-10-226-629A-496	Sequence 496, App
29	28	44.4	14	14	US-10-226-629A-509	Sequence 509, App
30	28	44.4	14	14	US-10-226-629A-521	Sequence 521, App
31	28	44.4	14	14	US-10-226-629A-532	Sequence 532, App
32	28	44.4	14	14	US-10-226-629A-542	Sequence 542, App
33	28	44.4	14	14	US-10-226-629A-551	Sequence 551, App
34	27	42.9	8	14	US-10-226-629A-464	Sequence 464, App
35	27	42.9	9	14	US-10-226-629A-465	Sequence 465, App
36	27	42.9	10	10	US-09-572-404B-18	Sequence 18, Appl
37	27	42.9	10	14	US-10-226-629A-466	Sequence 466, App
38	27	42.9	11	14	US-10-226-629A-467	Sequence 467, App
39	27	42.9	12	14	US-10-254-446A-165	Sequence 165, App
40	27	42.9	12	14	US-10-226-629A-468	Sequence 468, App
41	27	42.9	13	14	US-10-226-629A-469	Sequence 469, App
42	27	42.9	14	14	US-10-226-629A-470	Sequence 470, App
43	26	41.3	8	15	US-10-149-138-2763	Sequence 2763, Ap
44	26	41.3	8	16	US-10-149-138-2763	Sequence 2763, Ap
45	26	41.3	10	10	US-09-572-404B-1153	Sequence 1153, Ap

ALIGNMENTS

RESULT 1
US-10-194-441A-7
; Sequence 7, Application US/10194441A
; Publication No. US20030148944A1
; GENERAL INFORMATION:
; APPLICANT: Holmdahl, Rikard
; APPLICANT: Engstrom, Jan Ake
; APPLICANT: Kihlberg, Jan
; APPLICANT: Burkhardt, Harald
; TITLE OF INVENTION: TRIPLE POLYPEPTIDE COMPLEXES
; FILE REFERENCE: 11145-010001
; CURRENT APPLICATION NUMBER: US/10/194,441A
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 60/305,048
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-441A-7

Query Match 46.0%; Score 29; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7
Db 6 GERFP 10

RESULT 2
US-10-226-629A-477
; Sequence 477, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.

```

; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 477
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-477
```

```

Query Match      44.4%; Score 28; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY      4 ERFPDENF 11
      ::|||
Db      1 KKYPDINF 8
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```

RESULT 3
US-09-988-493-293
; Sequence 293, Application US/09988493
; Publication No. US20030064419A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-293
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```

Query Match      44.4%; Score 28; DB 12; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 FPDENF 11
      |||||
Db      1 FEDENF 6
```

```

RESULT 4
US-10-014-340-209
; Sequence 209, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
```

```

; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 209
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-209
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```

Query Match      44.4%; Score 28; DB 12; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 FPDENF 11
      |||||
Db      1 FEDENF 6
```

```

RESULT 5
US-10-226-629A-478
; Sequence 478, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 478
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-478
```

```

Query Match      44.4%; Score 28; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ERFPDENF 11
      ::|||
Db      1 KKYPDINF 8
```

```

RESULT 6
US-10-226-629A-491
; Sequence 491, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 491
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-491
```

Query Match 44.4%; Score 28; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0;

QY 4 ERFPDENF 11
Db 2 KKYPDLENF 9

RESULT 7

US-10-264-309-118
; Sequence 118, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-118

Query Match 44.4%; Score 28; DB 16; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPDENF 11
Db 1 FEDENF 6

RESULT 8

US-10-226-629A-479
; Sequence 479, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavit, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-479

Query Match 44.4%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
Db 1 KKYPDLENF 8

RESULT 9

US-10-226-629A-492
; Sequence 492, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavit, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 492
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-492

Query Match 44.4%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
Db 2 KKYPDLENF 9

RESULT 10

US-10-226-629A-505
; Sequence 505, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavit, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 505
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-505

Query Match 44.4%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11

Db 3 KKPDLNF 10

RESULT 11

US-10-226-629A-480
; Sequence 480, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 480
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-480

Query Match 44.4%; Score 28; DB 14; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDENF 11

Db 1 KKPDLNF 8

RESULT 12

US-10-226-629A-493
; Sequence 493, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 493
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-493

Query Match 44.4%; Score 28; DB 14; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDENF 11

Db 2 KKPDLNF 9

RESULT 13

US-10-226-629A-506
; Sequence 506, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

; FILE REFERENCE: 5006.01

; CURRENT APPLICATION NUMBER: US/10/226,629A

; CURRENT FILING DATE: 2002-08-22

; PRIOR APPLICATION NUMBER: US 60/314,182

; PRIOR FILING DATE: 2001-08-22

; NUMBER OF SEQ ID NOS: 736

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 506

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Variola virus

US-10-226-629A-506

Query Match 44.4%; Score 28; DB 14; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDENF 11

Db 3 KKPDLNF 10

RESULT 14

US-10-226-629A-518
; Sequence 518, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 518
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-518

Query Match 44.4%; Score 28; DB 14; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDENF 11

Db 4 KKPDLNF 11

RESULT 15

US-10-286-457-432
; Sequence 432, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 432
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-432

Query Match 44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGERFP 7
:| | |
Db 3 VYGNRLP 9

RESULT 16
US-10-226-629A-481
; Sequence 481, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 481
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-481

Query Match 44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | |
Db 1 KKYPDLPF 8

RESULT 17
US-10-226-629A-494
; Sequence 494, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 494
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-494

Query Match 44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | |
Db 2 KKYPDLPF 9

RESULT 18
US-10-226-629A-507
; Sequence 507, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 507
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-507

Query Match 44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | |
Db 3 KKYPDLPF 10

RESULT 19
US-10-226-629A-519
; Sequence 519, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 519
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-519

Query Match 44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | |
Db 4 KKYPDLPF 11

US-10-226-629A-519


```
RESULT 20
US-10-226-629A-530
; Sequence 530, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 530
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-530

Query Match      44.4%; Score 28; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENE 11
      :::|||
Db      5 KKYPDLEF 12

RESULT 21
US-10-226-629A-482
; Sequence 482, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 482
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-482

Query Match      44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENE 11
      :::|||
Db      1 KKYPDLEF 8

RESULT 22
US-10-226-629A-495
; Sequence 495, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
```

```
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 495
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-495

Query Match      44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENE 11
      :::|||
Db      2 KKYPDLEF 9

RESULT 23
US-10-226-629A-508
; Sequence 508, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 508
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-508

Query Match      44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENE 11
      :::|||
Db      3 KKYPDLEF 10

RESULT 24
US-10-226-629A-520
; Sequence 520, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 520
```

LENGTH: 13
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-520

Query Match 44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
: : : : :
Db 4 KKYPD LNF 11

RESULT 25

US-10-226-629A-531
Sequence 531, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 531
LENGTH: 13
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-531

Query Match 44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
: : : : :
Db 5 KKYPD LNF 12

RESULT 26

US-10-226-629A-541
Sequence 541, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 541
LENGTH: 13
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-541

Query Match 44.4%; Score 28; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
: : : : :
Db 6 KKYPD LNF 13

RESULT 27

US-10-226-629A-483
Sequence 483, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 483
LENGTH: 14
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-483

Query Match 44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
: : : : :
Db 1 KKYPD LNF 8

RESULT 28

US-10-226-629A-496
Sequence 496, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
PRIOR FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 496
LENGTH: 14
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-496

Query Match 44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
: : : : :
Db 2 KKYPD LNF 9

RESULT 29

US-10-226-629A-509
Sequence 509, Application US/10226629A
Publication No. US20030166504A1

```

; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 509
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-509
```

```

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ERFPDENF 11
        ::|||
Db       3 KKYPDLNF 10
```

```

RESULT 30
US-10-226-629A-521
; Sequence 521, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 521
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-521
```

```

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ERFPDENF 11
        ::|||
Db       4 KKYPDLNF 11
```

```

RESULT 31
US-10-226-629A-532
; Sequence 532, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
```

```

; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 532
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-532
```

```

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ERFPDENF 11
        ::|||
Db       5 KKYPDLNF 12
```

```

RESULT 32
US-10-226-629A-542
; Sequence 542, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 542
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-542
```

```

Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 ERFPDENF 11
        ::|||
Db       6 KKYPDLNF 13
```

```

RESULT 33
US-10-226-629A-551
; Sequence 551, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 551
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-551
```

```
Query Match      44.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 ERFPDENF 11
      :|||
Db      7 KYPDLNF 14

RESULT 34
US-10-226-629A-464
; Sequence 464, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 464
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-464

Query Match      42.9%; Score 27; DB 14; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      5 RFPDENF 11
      :|||
Db      1 KYPDLNF 7

RESULT 35
US-10-226-629A-465
; Sequence 465, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 465
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-465

Query Match      42.9%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      5 RFPDENF 11
      :|||
Db      1 KYPDLNF 7
```

```
RESULT 36
US-09-572-404B-18
; Sequence 18, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Protpatent version 1.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DSC3 OR DSC4 at 716-725 and may interact with
US-09-572-404B-18

Query Match      42.9%; Score 27; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GERFPD 8
      :|||
Db      5 GKRPPE 10

RESULT 37
US-10-226-629A-466
; Sequence 466, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 466
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-466

Query Match      42.9%; Score 27; DB 14; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      5 RFPDENF 11
      :|||
Db      1 KYPDLNF 7

RESULT 38
US-10-226-629A-467
; Sequence 467, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
```

```

; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 467
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-467

```

```

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 11;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 5 RPPDEF 11
Db 1 KYPDLF 7

```

```

RESULT 39
US-10-254-446A-165
; Sequence 165, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 165
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
US-10-254-446A-165

```

```

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 12;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 TYGERFPD 8
Db 1 LWGRFPD 8

```

```

RESULT 40
US-10-226-629A-468
; Sequence 468, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1

```

```

; SEQ ID NO 468
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-468

```

```

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 12;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 5 RPPDEF 11
Db 1 KYPDLF 7

```

```

RESULT 41
US-10-226-629A-469
; Sequence 469, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 469
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-469

```

```

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 13;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 5 RPPDEF 11
Db 1 KYPDLF 7

```

```

RESULT 42
US-10-226-629A-470
; Sequence 470, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 470
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-470

```

```

Query Match
Best Local Similarity 42.9%; Score 27; DB 14; Length 14;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 5 RFPDNE 11
:|||||
Db 1 KYPDLNF 7

RESULT 43
US-10-149-138-2763

; Sequence 2763, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2763
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
; US-10-149-138-2763

Query Match 41.3%; Score 26; DB 15; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPDE 9
:|||||
Db 1 KRPDE 5

RESULT 44
US-10-149-138-2763

; Sequence 2763, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2763
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
; US-10-149-138-2763

Query Match 41.3%; Score 26; DB 16; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RFPDE 9
:|||||
Db 1 KRPDE 5

RESULT 45
US-09-572-404B-1153

; Sequence 1153, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: Procpatent version 1.0
; SEQ ID NO 1153
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in BTM at 177-186 and may interact with Sequence
; US-09-572-404B-1153

Query Match 41.3%; Score 26; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7
:|||||
Db 6 GERFP 10

Search completed: August 30, 2004, 11:04:58
Job time : 14.4527 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 4.34797 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-6
Perfect score: 63
Sequence: 1 IYGERFPDENF 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	47.6	10	2	US-08-658-639-8 Sequence 8, Appli
2	30	47.6	10	3	US-08-944-604-8 Sequence 8, Appli
3	29	46.0	12	2	US-08-432-871C-99 Sequence 99, Appl
4	29	46.0	12	4	US-09-270-956-99 Sequence 99, Appl
5	28	44.4	13	1	US-07-923-724-57 Sequence 57, Appl
6	28	44.4	13	2	US-08-609-426A-57 Sequence 57, Appl
7	28	44.4	13	2	US-08-374-652C-44 Sequence 44, Appl
8	27	42.9	12	4	US-08-634-332A-77 Sequence 77, Appl
9	25	39.7	9	1	US-08-215-805A-27 Sequence 27, Appl
10	25	39.7	9	1	US-08-215-805A-44 Sequence 44, Appl
11	25	39.7	9	1	US-08-215-805A-54 Sequence 54, Appl
12	25	39.7	11	1	US-08-278-091-23 Sequence 23, Appl
13	25	39.7	11	1	US-08-483-859-23 Sequence 23, Appl
14	25	39.7	11	1	US-08-472-173-23 Sequence 23, Appl
15	25	39.7	11	2	US-08-487-167-23 Sequence 23, Appl
16	25	39.7	11	2	US-08-482-816-23 Sequence 23, Appl
17	25	39.7	11	2	US-08-296-149-23 Sequence 23, Appl
18	25	39.7	11	2	US-08-801-499-23 Sequence 23, Appl
19	25	39.7	11	2	US-08-615-271-23 Sequence 23, Appl
20	25	39.7	11	3	US-09-074-660-23 Sequence 23, Appl
21	25	39.7	11	3	US-09-074-659-23 Sequence 23, Appl
22	25	39.7	11	3	US-09-106-468-23 Sequence 23, Appl
23	25	39.7	11	3	US-09-106-466A-23 Sequence 23, Appl
24	25	39.7	11	3	US-09-106-467-23 Sequence 23, Appl
25	25	39.7	13	2	US-08-945-168-95 Sequence 95, Appl
26	25	39.7	13	4	US-08-999-689A-9 Sequence 9, Appli
27	25	39.7	14	2	US-08-945-168-94 Sequence 94, Appl

28	24	38.1	8	3	US-07-861-458C-115 Sequence 115, App
29	24	38.1	9	2	US-08-569-166-23 Sequence 23, Appl
30	24	38.1	9	2	US-08-522-269B-6 Sequence 6, Appli
31	24	38.1	9	3	US-09-294-923-6 Sequence 6, Appli
32	24	38.1	9	3	US-08-960-780-59 Sequence 59, Appl
33	24	38.1	9	3	US-09-073-898-59 Sequence 65, Appl
34	24	38.1	9	3	US-09-518-046-65 Sequence 79, Appl
35	24	38.1	9	3	US-09-518-046-79 Sequence 144, App
36	24	38.1	9	3	US-09-518-046-144 Sequence 51, Appl
37	24	38.1	9	4	US-09-618-259-51 Sequence 70, Appl
38	24	38.1	9	4	US-09-618-259-70 Sequence 59, Appl
39	24	38.1	9	4	US-09-850-351A-59 Sequence 3, Appli
40	24	38.1	10	1	US-08-151-574-3 Sequence 59, Appl
41	24	38.1	10	1	US-08-300-386A-59 Sequence 3, Appli
42	24	38.1	10	2	US-08-419-448-3 Sequence 59, Appl
43	24	38.1	10	3	US-08-931-645-59 Sequence 3, Appli
44	24	38.1	10	4	US-09-233-510-3 Sequence 4, Appli
45	24	38.1	10	5	PCT-US93-08067-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-658-639-8
; Sequence 8, Application US/08658639
; Patent No. 5914238
; GENERAL INFORMATION:
; APPLICANT: KEESSE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-YUE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,639
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-658-639-8

Query Match 47.6%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 RFPDENF 11
Db 1 KFDDENF 7

RESULT 2
US-08-944-604-8
Sequence 8, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: KESSEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-944-604-8

Query Match 47.6%; Score 30; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPDENF 11
Db 1 KFDENF 7

RESULT 3
US-08-432-871C-99
Sequence 99, Application US/08432871C
Patent No. 5877010
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-432-871C-99

Query Match 46.0%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGERFPDENF 11
Db 2 WGDHRPIEKF 11

RESULT 4
US-09-270-956-99
Sequence 99, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-270-956-99

Query Match 46.0%; Score 29; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 YGERFPDENF 11
:|:|:|:|
Db 2 WGDHRPIREKF 11

RESULT 5
US-07-923-724-57

; Sequence 57, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Palohelimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,724
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0240004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-07-923-724-57

Query Match 44.4%; Score 28; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGERFP 7
:|:|:|:|
Db 2 HGERYP 7

RESULT 6
US-08-609-426A-57

; Sequence 57, Application US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Palohelimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-609-426A-57

Query Match 44.4%; Score 28; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGERFP 7
:|:|:|:|
Db 2 HGERYP 7

RESULT 7
US-08-374-652C-44
; Sequence 44, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.

APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: FAGERSTROM, RICHARD B.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING, PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-374-652C-44

Query Match 44.4%; Score 28; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 YGERFP 7
DB 2 HGERYP 7

RESULT 8
US-08-634-332A-77
Sequence 77, Application US/08634332A
Patent No. 6531578
GENERAL INFORMATION:
APPLICANT: ROBERT WEBBER
TITLE OF INVENTION: MONOCLONAL ANTIBODY REACTIVE TO HUMAN INOS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIELEN, PETERSON & LAMPE
STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720

CITY: WALNUT CREEK
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94596
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,332A
FILING DATE: 12-Apr-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NONE
FILING DATE: NONE
ATTORNEY/AGENT INFORMATION:
NAME: THEODORE J. BIELEN, JR.
REGISTRATION NUMBER: 27,420
REFERENCE/DOCKET NUMBER: 12280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (925) 937-1515
TELEFAX: (925) 937-1529
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
FEATURE:
NAME/KEY: HUMAN INOS (1015-1026)
LOCATION: CARBOXY TERMINAL WITH AMIDE
IDENTIFICATION METHOD: AMINO ACID ANALYSIS
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-08-634-332A-77

Query Match 42.9%; Score 27; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 GERFPDEN 10
DB 1 GSRRPDED 8

RESULT 9
US-08-215-805A-27
Sequence 27, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
TITLE OF INVENTION: SUI5
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus actinomycetemcomitans
US-08-215-805A-27

Query Match 39.7%; Score 25; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERFPD 8
Db 2 YGSKFND 8

RESULT 10

US-08-215-805A-44
Sequence 44, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURRELLA
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-805A-44

Query Match 39.7%; Score 25; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGERFPD 9
:|:|:|

Db 1 LYGDKNDE 9

RESULT 11

US-08-215-805A-54
Sequence 54, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURRELLA
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-805A-54

Query Match 39.7%; Score 25; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERFPD 8
Db 2 FGSRFTD 8

RESULT 12

US-08-278-091-23
Sequence 23, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hln47 Protein with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario

COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-278-091-23

Query Match 39.7%; Score 25; DB 1; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 13
US-08-483-859-23
Sequence 23, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-859-23

Query Match 39.7%; Score 25; DB 1; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 14
US-08-472-173-23
Sequence 23, Application US/08472173
Patent No. 565353
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-493 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-472-173-23

Query Match 39.7%; Score 25; DB 1; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;

Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 15

US-08-487-167-23
; Sequence 23, Application US/08487167
; Patent No. 5869302
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: YANG, Yan-Ping
; APPLICANT: CHONG, Pele
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
; TITLE OF INVENTION: Reduced Protease Activity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,167
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/296,149
; FILING DATE: 26-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,091
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-508 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-487-167-23

Query Match 39.7%; Score 25; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 16

US-08-482-816-23
; Sequence 23, Application US/08482816
; Patent No. 5935573
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, Sheena M
; APPLICANT: YANG, Yan-Ping

APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-494 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-482-816-23

Query Match 39.7%; Score 25; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 17

US-08-296-149-23
; Sequence 23, Application US/08296149
; Patent No. 5939297
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, Sheena M
; APPLICANT: YANG, Yan-Ping
; APPLICANT: CHONG, Pele
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
; TITLE OF INVENTION: Reduced Protease Activity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-390
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-296-149-23

Query Match 39.7%; Score 25; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
Db 4 FGDRFAEQ 11

RESULT 18
US-08-801-499-23
Sequence 23, Application US/08801499
Patent No. 5962430
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus H1n47 Protein with Reduced Protease Act
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-671 MIS:jfb
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-801-499-23

Query Match 39.7%; Score 25; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
Db 4 FGDRFAEQ 11

RESULT 19
US-08-615-271-23
Sequence 23, Application US/08615271
Patent No. 5981503
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS H1N47 WITH REDUCED
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-580
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-615-271-23

Query Match 39.7%; Score 25; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
Db 4 FGDRFAEQ 11

RESULT 20

US-09-074-660-23
; Sequence 23, Application US/09074660
; Patent No. 6020183
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: YANG, Yan-Ping
; APPLICANT: CHONG, Pele
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Analog of Haemophilus HIN47 Protein with
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,660
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,167
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/296,149
; FILING DATE: 26-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,091
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-731 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-074-660-23

Query Match 39.7%; Score 25; DB 3; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
; :||| :
; Db 4 FGDRFAEQ 11

RESULT 21
US-09-074-659-23
; Sequence 23, Application US/09074659
; Patent No. 6025342
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: YANG, Yan-Ping
; APPLICANT: CHONG, Pele
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Analog of Haemophilus HIN47 Protein with
; TITLE OF INVENTION: Reduced Protease Activity

NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,167
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/296,149
; FILING DATE: 26-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,091
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-074-659-23

Query Match 39.7%; Score 25; DB 3; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
; :||| :
; Db 4 FGDRFAEQ 11

RESULT 22
US-09-106-468-23
; Sequence 23, Application US/09106468
; Patent No. 6114125
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: YANG, Yan-Ping
; APPLICANT: CHONG, Pele
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,468
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-825
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-106-468-23

Query Match 39.7%; Score 25; DB 3; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 23
US-09-106-466A-23
Sequence 23, Application US/09106466A
Patent No. 6147057
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,466A
FILING DATE:
CLASSIFICATION: 514514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION: 514514
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-826
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-106-466A-23

Query Match 39.7%; Score 25; DB 3; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 24
US-09-106-467-23
Sequence 23, Application US/09106467
Patent No. 6153580
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,467
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-106-467-23

Query Match 39.7%; Score 25; DB 3; Length 11;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 YGERFPDE 9
:|:|:|:
Db 4 FGDRFAEQ 11

RESULT 25
US-08-945-168-95
; Sequence 95, Application US/08945168
; Patent No. 5989548
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,168
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE96/00533
; FILING DATE: 23-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9501512-9
; FILING DATE: 24-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-945-168-95

Query Match 39.7%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFPDE 9
Db 3 GENVPDD 9

RESULT 26
US-08-999-689A-9
; Sequence 9, Application US/08999689A
; Patent No. 6541615
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: KHARITONENOV, ALEXEI
; APPLICANT: CHEN, ZHENGJUN
; TITLE OF INVENTION: SIRP PROTEINS AND USES THEREOF
; FILE REFERENCE: 038602/0548
; CURRENT APPLICATION NUMBER: US/08/999,689A
; FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/030,964
; PRIOR FILING DATE: 1996-11-15

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rattus sp.
US-08-999-689A-9

Query Match 39.7%; Score 25; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGERFP 7
Db 6 IGGERFP 12

RESULT 27
US-08-945-168-94
; Sequence 94, Application US/08945168
; Patent No. 5989548
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,168
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE96/00533
; FILING DATE: 23-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9501512-9
; FILING DATE: 24-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-945-168-94

Query Match 39.7%; Score 25; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GERFPDE 9
Db 4 GENVPDD 10

RESULT 28

US-07-861-458C-115
 ; Sequence 115, Application US/07861458C
 ; Patent No. 6232061
 ; GENERAL INFORMATION:
 ; APPLICANT: Marchionni, Mark Andrew
 ; APPLICANT: Johnson, Carl D.
 ; TITLE OF INVENTION: HOMOLOGY CLONING
 ; NUMBER OF SEQUENCES: 142
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/861,458C
 ; FILING DATE: 04/01/92
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 04585/014001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 115:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-07-861-458C-115

Query Match 38.1%; Score 24; DB 3; Length 8;
 Best Local Similarity 57.1%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGERFPD 8
 ||: ||
 Db 1 YGDCVPD 7

RESULT 29

US-08-569-166-23
 ; Sequence 23, Application US/08569166
 ; Patent No. 5830722
 ; GENERAL INFORMATION:
 ; APPLICANT: NICOLAS, LUC
 ; APPLICANT: CHARLES, JEAN-FRANCOIS
 ; APPLICANT: DELECTUSE, ARMELE
 ; APPLICANT: BARLOV, FREDERIQUE
 ; TITLE OF INVENTION: CLOSTRIDIUM BIFERMENTANS DNA FRAGMENT
 ; TITLE OF INVENTION: BEARING GENES CODING FOR PROTEINS LINKED TO AN
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/569,166
 ; FILING DATE: 05-JUL-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR94/00768
 ; FILING DATE: 24-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 93/07795
 ; FILING DATE: 25-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 660-106-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-569-166-23

Query Match 38.1%; Score 24; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 IYGERFPD 8
 ||||| ||
 Db 4 IYGE--PD 9

RESULT 30

US-08-522-269B-6
 ; Sequence 6, Application US/08522269B
 ; Patent No. 5919690
 ; GENERAL INFORMATION:
 ; APPLICANT: Knap, Inge Helmer
 ; APPLICANT: Hjort, Carsten M.
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Kofod, Lene Venke
 ; TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5919690 of No. 5919690th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/522,269B
 ; FILING DATE: 12-SEP-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gregg, Valeta A.
 ; REGISTRATION NUMBER: 37,125
 ; REFERENCE/DOCKET NUMBER: 3935,204-US
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-522-269B-6

Query Match 38.1%; Score 24; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFPD 8
Db 3 RFPD 6

RESULT 31

US-09-294-923-6
Sequence 6, Application US/09294923
Patent No. 6197566
GENERAL INFORMATION:
APPLICANT: Knap, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofod, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61975660 No. 6197566disk of No. 6197566ch America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,923
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/522,269
FILING DATE: 12-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-294-923-6

Query Match 38.1%; Score 24; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFPD 8
Db 3 RFPD 6

RESULT 32

US-08-960-780-59
Sequence 59, Application US/08960780
Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feitelson, Gerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-960-780-59

Query Match 38.1%; Score 24; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PDEN 10
Db 1 PDEN 4

RESULT 33

US-09-073-898-59
Sequence 59, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Feitelson, Gerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James

APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073, 898
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029, 848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960, 780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-073-898-59

Query Match 38.1%; Score 24; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDEN 10
Db 1 PDEN 4

RESULT 34
US-09-518-046-65
Sequence 65, Application US/09518046
Patent No. 6294663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518, 046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261, 416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 65
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: 328...336
OTHER INFORMATION: TADG-12 peptide
US-09-518-046-65

Query Match 38.1%; Score 24; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
Db 4 ENFPD 8

RESULT 35
US-09-518-046-79
Sequence 79, Application US/09518046
Patent No. 6294663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518, 046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261, 416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 79
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: 329...337
OTHER INFORMATION: TADG-12 peptide
US-09-518-046-79

Query Match 38.1%; Score 24; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
Db 3 ENFPD 7

RESULT 36
US-09-518-046-144
Sequence 144, Application US/09518046
Patent No. 6294663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518, 046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261, 416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 144
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: 330...338
OTHER INFORMATION: TADG-12 peptide
US-09-518-046-144

Query Match 38.1%; Score 24; DB 3; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
| | | |
Db 2 ENFPD 6

RESULT 37
US-09-618-259-51

; Sequence 51, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 162-170 of the TADG-14 protein
US-09-618-259-51

Query Match 38.1%; Score 24; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
| | | |
Db 4 ENFPD 8

RESULT 38

US-09-618-259-70
; Sequence 70, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 70
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 164-172 of the TADG-14 protein
US-09-618-259-70

Query Match 38.1%; Score 24; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPD 8
| | | |
Db 2 ENFPD 6

RESULT 39
US-09-850-351A-59

; Sequence 59, Application US/09850351A
; Patent No. 6656908
; GENERAL INFORMATION:
; APPLICANT: Feltelson, Jerald S.
; Schnepf, H. Ernest
; Narva, Kenneth E.
; Stockhoff, Brian A.
; Schmeits, James
; Loewer, David
; Dullum, Charles Joseph
; Muller-Cohn, Judy
; Stamp, Lisa
; Morrill, George

TITLE OF INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins

NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-850-351A-59

Query Match 38.1%; Score 24; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PDEN 10
| | | |
Db 1 PDEN 4

RESULT 40
US-08-151-574-3

; Sequence 3, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon

APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-151-574-3

Query Match 38.1%; Score 24; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGERFP 7
Db 1 VVDERFP 7

RESULT 41
US-08-300-386A-59
Sequence 59, Application US/08300386A
Patent No. 5667988
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F, III
APPLICANT: Burton, Dennis R
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,386A
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 409.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-300-386A-59

Query Match 38.1%; Score 24; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFP 7
Db 3 YGKRSP 8

RESULT 42
US-08-419-448-3
Sequence 3, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-APR-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-419-448-3

Query Match 38.1%; Score 24; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGERFP 7
Db 1 VDERFP 7

RESULT 43
US-08-931-645-59

Sequence 59, Application US/08931645
Patent No. 6096551

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F, III

APPLICANT: Burton, Dennis R

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES

TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute

STREET: 10666 No. 6096551th Torrey Pines Road, TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/931,645

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/300,386

FILING DATE: 02-SEP-1994

APPLICATION NUMBER: US 08/174,674

FILING DATE: 28-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/826,623

FILING DATE: 27-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/012,566

FILING DATE: 02-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 409.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-931-645-59

Query Match 38.1%; Score 24; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGERFP 7
Db 3 YGKRSP 8

RESULT 44

US-09-233-510-3

Sequence 3, Application US/09233510

Patent No. 6350602

GENERAL INFORMATION:

APPLICANT: Robert F.M. Van Gorcom

APPLICANT: Willem Van Hartingsveldt

APPLICANT: Petrus A. Van Paridon

APPLICANT: Annemarie E. Veenstra

APPLICANT: Rudolf G.M. Luttin

APPLICANT: Gerardus Selten

TITLE OF INVENTION: Cloning and Expression of Microbial

TITLE OF INVENTION: Phytase

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 545 Middlefield Road, Suite 200

CITY: Menlo Park

STATE: California

COUNTRY: USA

ZIP: 94025-3471

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,510

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/688,578

FILING DATE: 24-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 24615-20026.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-327-7250

TELEFAX: 415-327-2951

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

US-09-233-510-3

Query Match 38.1%; Score 24; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 IYGERFP 7
: ||||
Db 1 VVDERFP 7

RESULT 45

PCT-US93-08067-4

; Sequence 4, Application PC/TUS9308067

; GENERAL INFORMATION:

APPLICANT: Silva, Robert F

APPLICANT: Reilly, John D

TITLE OF INVENTION: PORTABLE INTRON AS AN INSERTION VECTOR FOR

TITLE OF INVENTION: GENE INSERTION

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern

STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 20004-2201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08067

FILING DATE: 27-AUG-1993

CLASSIFICATION: 435/235

CLASSIFICATION: C12N 7/00

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Application No. 07/936,423

FILING DATE: 27-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Holman, John C.

REGISTRATION NUMBER: 22,769

REFERENCE/DOCKET NUMBER: 043813PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666

TELEFAX: (202) 393-5350

TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-08067-4

Query Match 38.1%; Score 24; DB 5; Length 10;

Best Local Similarity 50.0%; Pred. No. 4.2e+02;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 FPDENF 11
: | : ||
Db 4 YPDNMF 9

Search completed: August 30, 2004, 10:57:16
Job time : 5.34797 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 16.3885 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-6
Perfect score: 63
Sequence: 1 IYGERFPDENF 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	63	100.0	11	3	AAy69926	Aay69926 Human cyc
2	41	65.1	9	3	AAy69927	Aay69927 Human cyc
3	31	49.2	10	7	ADA06843	Ada06843 Solid-pha
4	30	47.6	10	2	AAw44362	Aaw44362 Breast ca
5	30	47.6	10	4	AAb98714	Aab98714 Human bre
6	30	47.6	13	7	ADD23953	Add23953 Breast ca
7	29	46.0	10	7	ADC21550	Adc21550 Human col
8	29	46.0	12	2	AAy07435	Aay07435 HSV-1 TK
9	29	46.0	12	2	AAW97167	Aaw97167 HSV-1 TK
10	29	46.0	12	4	AAb86216	Aab86216 S. chryso
11	29	46.0	12	6	ABG99226	Abg99226 Thymidine
12	28	44.4	8	7	ADC43381	Adc43381 Variola s
13	28	44.4	9	4	AAU68482	Aau68482 Human Bre
14	28	44.4	9	4	AAb84975	Aab84975 Clone 2 s
15	28	44.4	9	5	ABG67487	Abg67487 Human ADP
16	28	44.4	9	6	ABR58800	AbR58800 Alzheimer
17	28	44.4	9	6	ADA23600	Ada23600 Alzheimer
18	28	44.4	9	7	ABR62869	AbR62869 Tumourige
19	28	44.4	9	7	ADC43382	Adc43382 Variola s
20	28	44.4	9	7	ADC43395	Adc43395 Variola s
21	28	44.4	10	7	ADC43396	Adc43396 Variola s
22	28	44.4	10	7	ADC43409	Adc43409 Variola s
23	28	44.4	10	7	ADC43383	Adc43383 Variola s
24	28	44.4	11	7	ADC43397	Adc43397 Variola s
25	28	44.4	11	7	ADC43410	Adc43410 Variola s

26	28	44.4	11	7	ADC43384	Adc43384 Variola s
27	28	44.4	11	7	ADC43422	Adc43422 Variola s
28	28	44.4	12	7	ADC43411	Adc43411 Variola s
29	28	44.4	12	7	ADC43385	Adc43385 Variola s
30	28	44.4	12	7	ADC43423	Adc43423 Variola s
31	28	44.4	12	7	ADC43434	Adc43434 Variola s
32	28	44.4	12	7	ADC43398	Adc43398 Variola s
33	28	44.4	12	7	ADC44703	Adc44703 Endothe li
34	28	44.4	12	7	ADC36084	Adc36084 Chemokine
35	28	44.4	13	2	AAr46829	Aar46829 pH 2.5 ac
36	28	44.4	13	7	AAr46829	AAr46829 pH 2.5 ac
37	28	44.4	13	7	ADC43424	Adc43424 Variola s
38	28	44.4	13	7	ADC43399	Adc43399 Variola s
39	28	44.4	13	7	ADC43412	Adc43412 Variola s
40	28	44.4	13	7	ADC43435	Adc43435 Variola s
41	28	44.4	13	7	ADC43386	Adc43386 Variola s
42	28	44.4	14	7	ADC43436	Adc43436 Variola s
43	28	44.4	14	7	ADC43387	Adc43387 Variola s
44	28	44.4	14	7	ADC43413	Adc43413 Variola s
45	28	44.4	14	7	ADC43425	Adc43425 Variola s

ALIGNMENTS

RESULT 1

AAy69926 standard; peptide; 11 AA.

AAy69926;

11-APR-2000 (first entry)

Human cyclophilin B peptide fragment #6.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

HLA antigen; diagnosis; tumour; therapy.

Homo sapiens.

WO9967288-A1.

29-DEC-1999.

24-JUN-1999; 99WO-JP003360.

25-JUN-1998; 98JP-00178449.

(SUMU) SUMITOMO PHARM CO LTD.

(ITOH/) ITOH K.

Itoh K, Gomi S;

WPI; 2000-116932/10.

Tumour antigen peptides derived from cyclophilin B for treatment and

diagnosis of tumours.

Claim 4; Page 50; 64pp; Japanese.

This sequence represents a cyclophilin B peptide of the invention. The

peptides are tumour antigen peptides derived from cyclophilin B, that

recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The

peptides are used for the treatment and diagnosis of tumours

Sequence 11 AA;

Query Match 100.0%; Score 63; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00025;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 IYGERPDENF 11

RESULT 2
AAV69927
ID AAV69927 standard; peptide; 9 AA.
XX
AC AAV69927;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #7.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumour antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 65.1%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFPDENF 11
Db 1 RFPDENF 7

RESULT 3
ADA06843
ID ADA06843 standard; peptide; 10 AA.
XX
AC ADA06843;
XX
DT 06-NOV-2003 (first entry)
XX
DE Solid-phase synthesis produced organic peptide #5.
XX
KW Aldehyde functionalised support material; solid-phase synthesis;
KW organic compound; acid; thioacid; thioester; alcohol;
KW disubstituted amide; aldehyde.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER

FT /note= "OTHER= "Fmoc-Arg"
FT Misc-difference 2
FT /note= "D-form residue"
FT Modified-site 10
FT /label= OTHER
FT /note= "OTHER= "Ala-OAl"
XX
PN US6566494-B1.
XX
PD 20-MAY-2003.
XX
PF 11-MAY-1999; 99US-00309828.
XX
PR 18-JUN-1996; 96US-00665509.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Jensen KJ, Barany G, Songster MF, Albericio F, Alsina J;
PI Vagner J;
XX
DR WPI; 2003-596202/56.
XX
PT New aldehyde functionalized support material used for solid phase organic
PT synthesis.
XX
PS Example 14; Col 18; 18pp; English.
XX
CC The invention is related to an aldehyde functionalised support material.
CC The aldehyde functionalised support material is used for solid-phase
CC synthesis of organic compounds, particularly peptides. The organic
CC compounds can have a variety of C-terminal functionalities e.g. acids,
CC thioacids, thioesters, alcohols, disubstituted amides and aldehydes can
CC be produced. This sequence represents an organic peptide prepared by
CC solid-phase synthesis, using the support material of the invention.
XX
SQ Sequence 10 AA;

Query Match 49.2%; Score 31; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 98;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 RFPDENF 11
Db 1 RFPEDNY 7

RESULT 4
AAW44362
ID AAW44362 standard; peptide; 10 AA.
XX
AC AAW44362;
XX
DT 28-MAY-1998 (first entry)
XX
DE Breast cancer-associated protein fragment BC-8 SEQ ID NO:8.
XX
KW Human; breast cancer-associated protein; nuclear matrix protein;
KW detection; diagnosis; antibody.
XX
OS Homo sapiens.
XX
PN WO9746884-A1.
XX
PD 11-DEC-1997.
XX
PF 03-JUN-1997; 97WO-US009529.
XX
PR 05-JUN-1996; 96US-00658639.
XX
PA (MATR-) MATRITECH INC.
XX
PI Keesee SK, Obar R, Wu Y;
XX

DR WPI; 1998-042336/04.

XX Diagnosing breast cancer by detecting a breast cancer-associated protein
PT - allows early and reliable diagnosis and treatment monitoring, and
PT antibody or inhibitory compounds useful for treating breast cancer.

PS Claim 10; Page 30; 47pp; English.

CC The present sequence represents a breast cancer-associated protein
CC fragment for use in a method for diagnosing breast cancer in tissue or
CC body fluid by detecting one or more breast cancer-associated protein(s).
CC Alternatively a nucleic acid encoding a breast cancer-associated protein
CC is detected in the sample by the use of a nucleic acid probe. The breast
CC cancer-associated proteins, encoding nucleic acids and antibodies are
CC useful in diagnostic assays and kits for breast cancer detection. The
CC proteins are also useful in screening for inhibitory compounds and
CC monitoring effectiveness of treatments. The antibody, or pharmaceutical
CC compositions containing the antibody or the inhibitory compound, can be
CC administered to patients to treat breast cancer. The methods allow
CC reliable and early diagnosis of breast cancer, or prediction of its
CC onset, by detection of specific markers expressed in breast tumour cells
CC but not in non-cancerous breast cells

CC Sequence 10 AA;

QY Query Match 47.6%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPDENF 11
:| |||||
Db 1 KFPDENF 7

RESULT 5
AAB98714
ID AAB98714 standard; peptide; 10 AA.

AC AAB98714;

DT 29-AUG-2001 (first entry)

DE Human breast cancer-associated protein BC-8 peptide, SEQ ID NO:8.

KW Human breast cancer-associated protein; BC-8; marker protein;
KW nuclear matrix protein; diagnosis; detection; tumour.

OS Homo sapiens.

PN US6218131-B1.

PD 17-APR-2001.

PF 06-OCT-1997; 97US-00944604.

PR 05-JUN-1996; 96US-00658639.

PA (MATR-) MATRITECH INC.

PI Keesee SK, Obar R, Wu Y;

DR WPI; 2001-396355/42.

PT Diagnosing or detecting breast cancer in an individual comprises
PT detecting the presence of breast cancer-associated proteins in a
PT biological sample.

PS Claim 9; Col 8; 30pp; English.

CC The invention relates to novel human breast cancer-associated proteins,
CC and their use in diagnosing and detecting breast cancer. The breast
CC cancer-associated proteins of the invention are nuclear matrix proteins
CC designated BC-2 (AAB98720), BC-8 isoform A (BC-8A, AAB98721) and CC BC-8

CC isoform B (BC-8B, AAB98722), although 6 other breast cancer-associated
CC nuclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were
CC also isolated (sequences not given in the specification). The novel
CC breast cancer-associated proteins are present in the nuclear matrix of
CC breast cancer cells, but are not present in the nuclear matrix of cells
CC from normal breast tissue. The invention also encompasses fragments of
CC the breast cancer-associated proteins (AAB98709-AAB98716), and methods
CC for their use in breast cancer diagnosis. The breast cancer marker
CC proteins of the invention or fragments thereof may be detected in a
CC sample of breast tissue or blood from an individual. Isolated breast
CC cancer-associated proteins may also be used to prepare antibodies,
CC particularly monoclonal antibodies, which may be used to detect or
CC diagnose breast cancer. Nucleic acids encoding the breast cancer-
CC associated proteins may also be used in the diagnosis and detection of
CC breast cancer, and in the isolation of DNA or protein sequences which may
CC interact with breast cancer-associated nuclear matrix proteins. Sequences
CC AAB98712-AAB98716 represent specifically claimed fragments of breast
CC cancer-associated protein BC-8

CC Sequence 10 AA;

QY Query Match 47.6%; Score 30; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RFPDENF 11
:| |||||
Db 1 KFPDENF 7

RESULT 6
ADD23953
ID ADD23953 standard; peptide; 13 AA.

AC ADD23953;

DT 15-JAN-2004 (first entry).

DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:928.

KW breast cancer; screening; diagnosis; breast cancer therapy;

KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.

OS Homo sapiens.

PN WO2003087831-A2.

PD 23-OCT-2003.

PF 10-APR-2003; 2003WO-GB001559.

PR 11-APR-2002; 2002GB-00008331.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Hudson LJ, Stamps AC, Terrett JA;

DR WPI; 2003-845381/78.

PT Screening, diagnosing and/or treating breast cancer by detecting a change
PT in expression or activity of a breast cancer membrane protein (BCMP)
PT polypeptide or encoding nucleic acid molecule.

PS Example; SEQ ID NO 928; 81pp; English.

CC The present invention describes a method of screening for and/or
CC diagnosing breast cancer in a subject, and/or monitoring the
CC effectiveness of breast cancer therapy. The method comprises detecting
CC and/or quantifying in a biological sample obtained from the subject a
CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
CC molecule. Also described: (1) an antibody, its functionally-active
CC fragment, derivative or analogue, that specifically binds to one or more
CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture

reagent specific for an BCMP polypeptide, reagents and instructions for use; (3) a method for screening for anti-breast cancer agents that interact with the BCMP polypeptide, comprising contacting the polypeptide with a candidate agent, and determining whether or not the candidate agent interacts with the polypeptide; (4) a method for screening for anti-breast cancer agents that modulate the expression or activity of an BCMP polypeptide or the nucleic acid molecule cited above, comprising comparing the expression or activity of the polypeptide or nucleic acid molecule, in the presence and absence of a candidate agent or in the presence of a control agent, and determining whether the candidate agent causes the expression or activity of the polypeptide or nucleic acid molecule to change; and (5) an agent identified by the method of (3) or (4), which interacts with the polypeptide or causes the expression or activity of the polypeptide, or the expression of the nucleic acid molecule to change. BCMPs have cytostatic activities, and can be used in vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or their derivatives, are useful in the manufacture of a medicament for the treatment of breast cancer, where the composition is a vaccine. The present sequence represents a BCMP peptide which is used in the exemplification of the present invention.

Sequence 13 AA;

Query Match 47.6%; Score 30; DB 7; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPPDEN 10
Db 1 ERFPPDEN 7

RESULT 7
ADCC21550

ID ADCC21550 standard; peptide; 10 AA.

AC ADCC21550;

DT 18-DEC-2003 (first entry)

DE Human collagen II epitope peptide SeqID7.

triple helix formation sequence; interpolypeptide linkage;
rheumatoid arthritis; autoimmune disease; inflammatory disease;
peripheral joint; major histocompatibility complex class II region;
HLA-DR; T cell; joint specific antigen; B cell; type II collagen; CII;
antiarthritic; antirheumatic; immunosuppressive; dermatological;
antiinflammatory; antipsoriatic; antiasmatic; neuroprotective;
relapsing polychondritis; systemic lupus erythematosus; psoriasis;
asthma; Sjogren's syndrome; multiple sclerosis; epitope peptide; human.

Homo sapiens.

WO2003006603-A2.

23-JAN-2003.

11-JUL-2002; 2002WO-IB004256.

12-JUL-2001; 2001US-0305048P.

(AREX-) AREXIS AB.

Holmdahl R, Burkhardt H, Engstrom JA, Kihlberg J;

WPI; 2003-221724/21.

Composition for treating autoimmune disorders such as rheumatoid arthritis, comprises three polypeptides, each comprising a triple helix formation sequence, and at least two interpolypeptide linkages.

Claim 17, SEQ ID NO 7, 113pp; English.

This invention relates to a novel composition comprising three polypeptides, where each polypeptide comprises a triple helix formation sequence and at least two interpolypeptide linkages such that each polypeptide is attached to at least one of the other two polypeptides. Rheumatoid arthritis is an autoimmune, inflammatory disease that affects peripheral joints. The main genetic association is to the major histocompatibility complex class II region (HLA-DR), suggesting that T cell mediated autoimmune recognition of joint specific antigens is involved in the disease. In addition, B cell mediated autoimmune responses have been observed in rheumatoid joints. Specifically, B cells have been detected secreting IgG antibodies specific for type II collagen (CII). The compounds of the invention may be antiarthritic, antirheumatic, immunosuppressive, dermatological, antiinflammatory, antipsoriatic, antiasmatic or vasoprotective through the enhancement of tolerance to the endogenous polypeptide. The compounds may be useful for diagnosing and treating autoimmune conditions such as rheumatoid arthritis, relapsing polychondritis, systemic lupus erythematosus, psoriasis, chronic stages of asthma, Jorg's syndrome and multiple sclerosis. The present sequence is that of a human type II collagen (CII) peptide epitope of the invention.

Sequence 10 AA;

Query Match 46.0%; Score 29; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERFP 7
Db 6 GERFP 10

RESULT 8
AAV07435

ID AAV07435 standard; peptide; 12 AA.

AC AAV07435;

DT 16-JUL-1999 (first entry)

DE HSV-1 TK amino acids 159-173 mutant #27.

HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme; pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis; viral disease; AIDS; hepatitis; parasite; bacterial infection.

Herpes simplex virus unknown type.

Synthetic.

WO9919466-A2.

22-APR-1999.

14-OCT-1998; 98WO-US021672.

14-OCT-1997; 97US-0061812P.

(DARW-) DARWIN MOLECULAR CORP.

Black ME;

WPI; 1999-277631/23.

New Herpesviridae thymidine kinase mutants - useful for treating prostate hypertrophy, allergies, cystic fibrosis and Alzheimer's disease.

Disclosure; Fig 15; 126pp; English.

This sequence represents a mutant form of amino acids 159-173 of the herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which was used to generate mutant TK proteins. The invention relates to the generation of novel HSV-1 TK or guanylate kinase (GK) genes with a

CC mutation upstream, within or downstream from a DRH nucleoside binding
 CC site. The TK enzymes can be used for inhibiting pathogenic agents, e.g.
 CC tumours, hyperkeratosis, psoriasis, prostate hypertrophy,
 CC hyperthyroidism, endocrinopathies, autoimmune diseases, allergies,
 CC restenosis, viral diseases such as AIDS, hepatitis, intracellular
 CC parasitic diseases or bacterial infection
 XX
 SQ Sequence 12 AA;

Query Match 46.0%; Score 29; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 YGERFPDENF 11
 :|:| | | |
 Db 2 WGDHRPIEKF 11

RESULT 9

AAW97167
 ID AAW97167 standard; peptide; 12 AA.

XX AAW97167;

DT 22-JUN-1999 (first entry)

DE HSV-1 TK amino acids 159-173 mutant #27.

XX HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme;
 KW pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy;
 KW hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis;
 KW viral disease; AIDS; hepatitis; parasite; bacterial infection.
 XX
 OS Herpes simplex virus unknown type.
 OS Synthetic.

XX US5877010-A.

XX 02-MAR-1999.

PF 02-MAY-1995; 95US-00432871.

PR 02-MAY-1994; 94US-00237592.

PA (UNIW) UNIV WASHINGTON.

PI Black ME, Loeb LA;

XX WPI; 1999-189650/16.

PT New Herpesviridae thymidine kinase mutant nucleic acids - used to
 PT develop products for treating e.g. tumours, autoimmune diseases,
 PT allergies, restenosis or viral, bacterial or parasitic diseases.
 XX

PS Disclosure; Fig 15; 72pp; English.

XX This sequence represents a mutant form of amino acids 159-173 of the
 CC herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which
 CC was used to generate mutant TK proteins. The invention relates to the
 CC generation of novel HSV-1 TK or guanylate kinase (GK) genes with a
 CC mutation upstream, within or downstream from a DRH nucleoside binding
 CC site. The TK enzymes can be used for inhibiting pathogenic agents, e.g.
 CC tumours, hyperkeratosis, psoriasis, prostate hypertrophy,
 CC hyperthyroidism, endocrinopathies, autoimmune diseases, allergies,
 CC restenosis, viral diseases such as AIDS, hepatitis, intracellular
 CC parasitic diseases or bacterial infection
 XX

SQ Sequence 12 AA;

Query Match 46.0%; Score 29; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 YGERFPDENF 11
 :|:| | | |
 Db 2 WGDHRPIEKF 11

RESULT 10

AA86216
 ID AA86216 standard; protein; 12 AA.

XX AA86216;

DT 31-AUG-2001 (first entry)

DE S. chrysomallus DABA acetyltransferase peptide fragment Ke15P6.

XX Tetrahydroxypyrimidine dioxigenase; thpd; probe; hydroxyectoine;
 KW 2-methyl-4-carboxy-5-hydroxy-3,4,5,6-tetrahydroxypyrimidine;
 KW hydroxylated tetrahydroxypyrimidine; DABA acetyltransferase.
 XX

OS Streptomyces chrysomallus.

XX WO200138500-A2.

PD 31-MAY-2001.

PF 17-NOV-2000; 2000WO-DE004036.

PR 24-NOV-1999; 99DE-01057470.

PA (ACTI-) ACTINODRUG PHARM GMBH.

PI Keller U;

DR WPI; 2001-381290/40.

XX New nucleic acid sequence encoding polypeptide having
 PT tetrahydroxypyrimidine-dioxigenase activity, useful in the production of
 PT hydroxylated tetrahydroxypyrimidines, in vivo or in vitro.
 XX

PS Disclosure; Fig 3; 25pp; German.

XX This invention describes a novel nucleic acid sequence (I), encoding a
 CC polypeptide having tetrahydroxypyrimidine-dioxigenase (thpd) activity. The
 CC products of the invention can be used as probes for the identification of
 CC chromosomal or extrachromosomal genes in Archaeobacteria, prokaryotes or
 CC eukaryotes which encode thpd and for the preparation of hydroxylated
 CC tetrahydroxypyrimidines. In particular the components having thpd activity
 CC are useful for producing hydroxylated tetrahydroxypyrimidine compounds such
 CC as 2-methyl-4-carboxy-5-hydroxy-3,4,5,6-tetrahydroxypyrimidine (ThpA);
 CC hydroxyectoine), in vivo or in vitro. The thpd polypeptides provide a
 CC simple, inexpensive method of preparing hydroxylated tetrahydroxypyrimidine
 CC compounds, which are difficult to prepare by chemical synthesis. This
 CC sequence represents a Streptomyces chrysomallus DABA acetyltransferase
 CC tryptic peptide fragment Ke15P6
 XX

SQ Sequence 12 AA;

Query Match 46.0%; Score 29; DB 4; Length 12;
 Best Local Similarity 71.4%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GERFPDE 9
 :|:| | | |
 Db 5 GELFPDE 11

RESULT 11

ABG99226
 ID ABG99226 standard; peptide; 12 AA.

XX ABG99226;

DT 15-JAN-2003 (first entry)

```
XX Thymidine kinase (TK) residues 159-173 mutant #29.
DE
XX
XX Herpesviridae; thymidine kinase; TK; DRH nucleoside binding region;
XX viral inhibitor; bacterial inhibitor; parasite inhibitor; tumour;
XX autotransactive immune cell; cancer; hyperkeratosis; psoriasis;
XX prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy;
XX autoimmune disease; restenosis; viral disease; AIDS; hepatitis; HCV; HBV;
XX acquired immunodeficiency syndrome; intracellular parasitic disease;
XX gene therapy; adenosine deaminase deficiency; Alzheimer's disease;
XX mutant; mutein.
XX
XX Herpesviridae.
OS Synthetic.
XX
XX US6451571-B1.
XX
XX 17-SEP-2002.
XX
XX 17-MAR-1999; 99US-00270956.
XX
XX 02-MAY-1994; 94US-00237592.
XX
XX 02-MAY-1995; 95US-00432871.
XX
XX 02-NOV-1995; 95US-00552304.
XX
XX (UNITW ) UNIV WASHINGTON.
XX
XX Loeb LA, Black ME;
XX
XX WPI; 2003-045581/04.
XX
XX Novel Herpesviridae thymidine kinase mutant useful for inhibiting
XX pathogens e.g. viruses, bacteria, tumor in animals, has one or more
XX mutations encoding amino acid substitutions upstream from the DRH
XX nucleoside binding site.
XX
XX
XX Disclosure; Col 91-92; 78pp; English.
XX
XX
XX The invention describes an isolated Herpesviridae thymidine kinase (TK)
XX comprising a 12 amino acid (aa) nucleoside binding region having a site 3
XX made up of a DRH nucleoside binding site and a site 4 and mutation(s), at
XX least one of the mutations being an aa substitution 2 or 3 aa upstream or
XX 5 or more aa downstream from the DRH motif that increases a biological
XX activity, preferably ability of TK to phosphorylate a nucleoside
XX analogue, as compared to unmutated TK. TK mutants are useful for
XX inhibiting a pathogenic agent such as viruses, bacteria, parasites,
XX tumour cells or autotransactive immune cells in a warm-blooded animal. TK
XX mutant is useful for inhibiting a tumour or cancer in a warm-blooded
XX animal, for treating a variety of disease e.g., hyperkeratosis
XX (psoriasis), prostate hypertrophy, hyperthyroidism, endocrinopathies,
XX autoimmune diseases, allergies, restenosis, viral diseases such as
XX acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV),
XX intracellular parasitic diseases, and to correct aberrant expression of a
XX gene within a cell, or to replace a specific gene which is defective in
XX proper expression using gene therapy, e.g. including adenosine deaminase
XX deficiency, and Alzheimer's diseases. The mutants are utilised as a
XX conditionally lethal marker for homologous recombination. This is the
XX amino acid sequence of a herpesviridae thymidine kinase (TK) mutant
XX peptide
XX
XX Sequence 12 AA;
SQ
Query Match 46.0%; Score 29; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 2 YGERPPDENF 11
DB 2 WGDHRPIERF 11
```

RESULT 12
ADC43381

```
ID ADC43381 standard; peptide; 8 AA.
XX
XX ADC43381;
AC
XX
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 477.
XX
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
XX herpes simplex virus; HSV; UL42 protein; variola virus A10L;
XX vaccinia virus virion core protein P4a;
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
XX viral budding; viral infectivity.
XX
XX Variola virus.
XX
XX WO2003017943-A2.
XX
XX 06-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027066.
XX
XX 22-AUG-2001; 2001US-0314182P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
XX Novel peptide, comprising a contiguous amino acid sequence of a viral
XX protein, capable of binding to a region of cellular protein AP-50 is
XX useful for treating viral infections.
XX
XX
XX Claim 31; SEQ ID NO 477; 60pp; English.
XX
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where
XX the contiguous amino acid sequence encompasses the YPXL motif of the
XX viral protein, and the 7-30 amino acid viral protein is capable of
XX binding a region including the amino acid residues 121-435 of cellular
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected
XX from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
XX protein, variola virus A10L protein, vaccinia virus virion core protein
XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
XX the contiguous amino acid sequence encompasses the YPXL motif of the viral
XX protein. The peptides of the invention are useful in the manufacture of a
XX medicament for treating viral infections caused by a virus selected from
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
XX viral budding from virus-infected cells and/or inhibiting viral
XX infectivity, thus inhibiting viral propagation in the cells. This
XX sequence represents a Variola smallpox virus A10L YPXL motif containing
XX peptide used in the treatment of viral infections of the invention.
XX
XX Sequence 8 AA;
SQ
Query Match 44.4%; Score 28; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 4 ERPPDENF 11
DB 1 KKYPDLNF 8
```

RESULT 13
AAU68482
ID AAU68482 standard; peptide; 9 AA.
XX
XX AAU68482;
AC
XX
DT 16-JAN-2002 (first entry)
XX

DE Human Breast cancer-associated protein isoform, BPI-270 peptide #2.
XX
KW Human; Breast cancer-associated protein isoform; breast cancer;
KW immunogen; cytostatic; BPI; tryptic digest peptide.
XX
OS Homo sapiens.
XX
PN WO200171357-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-GB001219.
XX
PR 20-MAR-2000; 2000GB-00006695.
PR 24-MAR-2000; 2000GB-00007265.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;
XX
DR WPI; 2001-611532/70.
XX
PT Identifying proteins for clinical screening, diagnosis and prognosis of
PT breast cancer, comprises detecting Breast Cancer-Associated Protein
PT isoforms (BPIs) using two-dimensional electrophoresis.
XX
PS Claim 9; Page 53; 197pp; English.
XX
CC The invention relates to diagnosing, determining the stage or severity,
CC or identifying the risk of a subject developing cancer (especially breast
CC cancer), or monitoring the effect of therapy on a subject with cancer,
CC comprising analysing a test sample using two-dimensional electrophoresis
CC and detecting Breast Cancer-Associated Protein isoforms (BPIs). The
CC methods disclosed are used for the diagnosis and prognosis of breast
CC cancer, for determining the severity of breast cancer, and for
CC identifying a subject at risk of developing breast cancer, and monitoring
CC the effect of therapy administered to a subject. Antibodies raised
CC against the binding domain of a BPI, the binding domain of a BPI, a
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
CC of a BPI can be incorporated into a pharmaceutical composition for
CC treating or preventing breast cancer. The methods use sensitive and
CC specific biomarkers provide early diagnosis of breast cancer, and the
CC compositions are more potent, specific, and has a more rapid effect with
CC fewer side effects than other prior art methods. The present sequence is
CC a tryptic digest peptide from a BPI of the invention
XX
SQ Sequence 9 AA;
XX
Query Match 44.4%; Score 28; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 PPDENF 11
Db 1 FEDENF 6
XX
RESULT 14
AAB84975
ID AAB84975 standard; protein; 9 AA.
XX
AC AAB84975;
XX
DT 06-AUG-2001 (first entry)
XX
DE Clone 2 scFv CDR L3 region binding to target antigen D.
XX
KW Antinflammatory; antiallergic; cytostatic; antibacterial; antiviral;
KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
KW antiarthritic; dermatological; immune response; modulator; enzyme;
KW antigen D; T-cell receptor; complementary determining region; CDR.
XX
OS Homo sapiens.

XX
PN WO200140312-A2.
XX
PD 07-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-GB004629.
XX
PR 03-DEC-1999; 99GB-00028789.
XX
PA (DIVE-) DIVERSYS LTD.
XX
PI Holt LJ, De Wildt RMT, Tomlinson I;
XX
DR WPI; 2001-374801/39.
XX
PT Isolating a polypeptide of interest from a naive polypeptide repertoire
PT which has not been preselected with a specific target ligand involves
PT direct screening of naive polypeptide repertoire with the target ligand.
XX
PS Example 2; Page 29; 41pp; English.
XX
CC The invention relates to isolating, from a naive polypeptide (I)
CC repertoire (antibody or T-cell receptor polypeptides), which has not been
CC preselected with a specific target ligand, a polypeptide of interest (II)
CC capable of interacting with the specific target ligand. The method
CC involves direct screening of (I) with the target ligand in order to
CC identify (II). The polypeptides selected by the method may be used in any
CC process which involves ligand-polypeptide binding including in vivo
CC therapeutic and prophylactic applications, in vitro and in vivo
CC diagnostic applications, in vitro assay and reagent applications. Enzyme
CC variants generated and selected by the method may be assayed for
CC activity, either in vitro or in vivo using standard techniques. Antibody
CC polypeptides selected by the method are used diagnostically in Western
CC analysis and in situ protein detection. The selected antibodies are
CC useful for preventing, suppressing or treating inflammatory states,
CC allergic hypersensitivity, cancer, bacterial or viral infection and
CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,
CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and
CC myasthenia gravis. The selected polypeptides may be used extracorporeally
CC or in vitro selectively to kill, deplete or effectively remove a target
CC cell population from a heterogeneous collection of cells. Sequences
CC AAB84968-979 represent complementary determining regions (CDRs) of scFv
CC heavy and light chains binding to target antigens M and D
XX
SQ Sequence 9 AA;
XX
Query Match 44.4%; Score 28; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 GERFPD 8
Db 3 GERFPD 8
XX
RESULT 15
ABG67487
ID ABG67487 standard; peptide; 9 AA.
XX
AC ABG67487;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human ADPI tryptic digest peptide #196.
XX
KW Human; Alzheimer's disease; AD; brain tissue; ADP; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX
OS Homo sapiens.
XX
PN WO200246767-A2.

XX 13-JUN-2002.
PD
XX
XX 29-NOV-2001; 2001WO-GB005289.
PF
XX 08-DEC-2000; 2000US-0254431P.
PR
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX WPI; 2002-508575/54.
DR
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.
XX
PS Claim 7; Page 72; 427pp; English.
XX
CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides
XX
SQ Sequence 9 AA;
QY
Db 6 FPDENF 11
1 FEDENF 6
Query Match 44.4%; Score 28; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 16
ABR58800
ID ABR58800 standard; peptide; 9 AA.
XX
AC ABR58800;
XX
DT 11-JUL-2003 (first entry)
XX
DE Alzheimer's Disease-associated protein isoform, API-333, SEQ ID 118.
XX
KW Nootropic; Neuroprotective; Alzheimer's disease; API; human;
KW Alzheimer's Disease-associated protein isoform.
XX
OS Homo sapiens.
XX
PN WO2003028543-A2.
XX
PD 10-APR-2003.
XX
PF 03-OCT-2002; 2002WO-US031642.
XX
PR 03-OCT-2001; 2001US-0326708P.
XX

PA (PFIZ) PFIZER PROD INC.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Durham UK, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stigler TR;
PI Sunderland PT, Townsend RR, White WF, Williams SA;
XX
DR WPI; 2003-371957/35.
XX
XX
PT Screening or diagnosing of Alzheimer's disease (AD) determine the stage
PT or severity of AD in a subject, comprises analyzing a test sample of body
PT fluid from the subject by 2-dimensional electrophoresis.
XX
PS Claim 2; Page 34; 179pp; English.
XX
CC The present invention relates to methods for screening or diagnosing
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a
CC subject, to identify subject at risk of developing AD, or to monitor the
CC effect of therapy administered. The methods comprise analysing a test
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-
CC dimensional array of AD-associated features (AFs). The method
CC alternatively comprises quantitatively detecting in a sample of body
CC fluid from the subject, one or more AD-associated protein isoforms (ADPIs;
CC ABR58710-ABR59184)
XX
SQ Sequence 9 AA;
QY
Db 6 FPDENF 11
1 FEDENF 6
Query Match 44.4%; Score 28; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 17
ADA23600
ID ADA23600 standard; peptide; 9 AA.
XX
AC ADA23600;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #209.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
DR WPI; 2003-540784/51.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX

PS Disclosure; SEQ ID NO 209; 115pp; English.

CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potentially, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.

XX
SQ Sequence 9 AA;

QY 6 FPDENF 11
| | | | |
1 FEDENF 6

Db 1 FEDENF 6

RESULT 18
ABR62869
ID ABR62869 standard; peptide; 9 AA.

XX ABR62869;
AC
DT 04-DEC-2003 (first entry)
XX
DE Tumorigenesis, metastasis-associated T cell cyclophilin peptide.
XX
KW Cyclophilin; peptidyl-prolyl cis-trans isomerase; enzyme; tumorigenesis;
XX metastasis; cancer; diagnosis; human.
OS Homo sapiens.
XX
PN WO2003060522-A1.
XX
PD 24-JUL-2003.
XX
PF 28-DEC-2002; 2002WO-KR002469.
XX
PR 29-DEC-2001; 2001KR-00088090.
XX
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI Ko JH, Hwang SY, Sohn H, Oh S, Lee JH, Lee SC, Yoo J, Lee D;
XX WPI; 2003-646050/61.
DR
XX
XX
PT Diagnosing cancers by measuring the changes of N-linked sugar chains of
PT proteins related to tumorigenesis and metastasis, including cancers of
PT the large intestine, stomach, lung, liver, uterus, breast and pancreas.
XX
PS Example 3; Page 42; 49pp; English.

XX
CC The present sequence is a peptide fragment of T cell cyclophilin
CC (peptidyl-prolyl cis-trans isomerase). Changes in glycosylation of this
CC protein are associated with metastasis and tumorigenesis. The protein
CC has 3 preserved N-linked sugar chain sites. A method for diagnosing
CC cancer involves measuring changes of sugar chains of proteins related to
CC tumorigenesis and metastasis. The changes are especially changes of sugar
CC chain branches of N-linked beta-1,6 N-acetylglucosamine. The protein is
CC prostate-derived factor, peptidyl-prolyl cis-trans isomerase, galectin
CC binding protein, L3 antigen, Mac-2-binding protein, serum protein 90K,
CC tumour associated antigen 90K, TIMP-1 and a novel, unidentified protein.

CC The cancer is large intestine cancer, stomach cancer, lung cancer, liver
CC cancer, uterine cancer, breast cancer and pancreas cancer

XX
SQ Sequence 9 AA;

QY 6 FPDENF 11
| | | | |
1 FEDENF 6

Db 1 FEDENF 6

RESULT 19
ADC43382
ID ADC43382 standard; peptide; 9 AA.

XX ADC43382;
AC
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 478.
XX
KW viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

OS Variola virus.
XX
PN WO2003017943-A2.
XX
PD 06-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027066.
XX
PR 22-AUG-2001; 2001US-0314182P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX WPI; 2003-371696/35.
DR
XX
PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

XX
PS Claim 31; SEQ ID NO 478; 60pp; English.

XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 9 AA;

QY Match 44.4%; Score 28; DB 7; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPDENF 11
Db 1 KKYPDLNF 8

RESULT 20

ADC43395
ID ADC43395 standard; peptide; 9 AA.

AC ADC43395;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 491.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;

KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 491; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid residues 121-435 of cellular
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

SQ Sequence 9 AA;

Query Match 44.4%; Score 28; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPDENF 11
Db 2 KKYPDLNF 9

RESULT 21
ADC43396
ID ADC43396 standard; peptide; 10 AA.

AC ADC43396;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 492.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 492; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid residues 121-435 of cellular
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

SQ Sequence 10 AA;

Query Match 44.4%; Score 28; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPDENF 11
Db 2 KKYPDLNF 9

RESULT 22
ADC43409
ID ADC43409 standard; peptide; 10 AA.

AC ADC43409;
XX
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 505.
XX
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.
XX
OS Variola virus.
XX
PN WO2003017943-A2.
XX
PD 06-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027066.
XX
PR 22-AUG-2001; 2001US-0314182P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
DR WPI; 2003-371696/35.
XX
PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.
XX
PS Claim 31; SEQ ID NO 505; 60pp; English.
XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
SQ Sequence 10 AA;
OY
Query Match 44.4%; Score 28; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 4 ERFPDENF 11
:::|||||
3 KKYPDLNF 10

RESULT 23
ADC43383
ID ADC43383 standard; peptide; 10 AA.
XX
AC ADC43383;
XX
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 479.
XX

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.
XX
OS Variola virus.
XX
PN WO2003017943-A2.
XX
PD 06-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027066.
XX
PR 22-AUG-2001; 2001US-0314182P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
DR WPI; 2003-371696/35.
XX
PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.
XX
PS Claim 31; SEQ ID NO 479; 60pp; English.
XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
SQ Sequence 10 AA;
OY
Query Match 44.4%; Score 28; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 4 ERFPDENF 11
:::|||||
1 KKYPDLNF 8

RESULT 24
ADC43397
ID ADC43397 standard; peptide; 11 AA.
XX
AC ADC43397;
XX
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 493.
XX
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.
XX

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OS Variola virus.
XX
XX WO2003017943-A2.
XX
XX 06-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027066.
XX
XX 22-AUG-2001; 2001US-0314182P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
XX Novel peptide, comprising a contiguous amino acid sequence of a viral
XX protein, capable of binding to a region of cellular protein AP-50 is
XX useful for treating viral infections.
XX
XX Claim 31; SEQ ID NO 493; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where
XX the contiguous amino acid sequence encompasses the YPXL motif of the
XX viral protein, and the 7-30 amino acid viral protein is capable of
XX binding a region including the amino acid residues 121-435 of cellular
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected
XX from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
XX protein, variola virus A10L protein, vaccinia virus virion core protein
XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
XX the contiguous amino acid sequence encompasses the YPXL motif of the viral
XX protein. The peptides of the invention are useful in the manufacture of a
XX medicament for treating viral infections caused by a virus selected from
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
XX viral budding from virus-infected cells and/or inhibiting viral
XX infectivity, thus inhibiting viral propagation in the cells. This
XX sequence represents a Variola smallpox virus A10L YPXL motif containing
XX peptide used in the treatment of viral infections of the invention.
XX
XX Sequence 11 AA;
SQ
Query Match 44.4%; Score 28; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 ERPPDENF 11
Db 2 KKYPDLNF 9
RESULT 25
ADC43410
ID ADC43410 standard; peptide; 11 AA.
XX
XX ADC43410;
AC
XX 18-DEC-2003 (first entry)
DT
XX
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 506.
DE
XX
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
XX herpes simplex virus; HSV; UL42 protein; variola virus A10L;
XX vaccinia virus virion core protein P4a;
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
XX viral budding; viral infectivity.
XX
XX Variola virus.
OS
XX WO2003017943-A2.
XX
XX 06-MAR-2003.
XX

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PF 22-AUG-2002; 2002WO-US027066.
XX
XX 22-AUG-2001; 2001US-0314182P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
XX Novel peptide, comprising a contiguous amino acid sequence of a viral
XX protein, capable of binding to a region of cellular protein AP-50 is
XX useful for treating viral infections.
XX
XX Claim 31; SEQ ID NO 506; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
XX amino acid sequence of 7-30 amino acid residues of a viral protein, where
XX the contiguous amino acid sequence encompasses the YPXL motif of the
XX viral protein, and the 7-30 amino acid viral protein is capable of
XX binding a region including the amino acid residues 121-435 of cellular
XX protein AP-50. The isolated 7-30 amino acid viral protein is selected
XX from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
XX protein, variola virus A10L protein, vaccinia virus virion core protein
XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
XX the contiguous amino acid sequence encompasses the YPXL motif of the viral
XX protein. The peptides of the invention are useful in the manufacture of a
XX medicament for treating viral infections caused by a virus selected from
XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
XX viral budding from virus-infected cells and/or inhibiting viral
XX infectivity, thus inhibiting viral propagation in the cells. This
XX sequence represents a Variola smallpox virus A10L YPXL motif containing
XX peptide used in the treatment of viral infections of the invention.
XX
XX Sequence 11 AA;
SQ
Query Match 44.4%; Score 28; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 ERPPDENF 11
Db 3 KKYPDLNF 10
RESULT 26
ADC43384
ID ADC43384 standard; peptide; 11 AA.
XX
XX ADC43384;
AC
XX 18-DEC-2003 (first entry)
DT
XX
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 480.
DE
XX
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
XX herpes simplex virus; HSV; UL42 protein; variola virus A10L;
XX vaccinia virus virion core protein P4a;
XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
XX viral budding; viral infectivity.
XX
XX Variola virus.
OS
XX WO2003017943-A2.
XX
XX 06-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027066.
XX
XX 22-AUG-2001; 2001US-0314182P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX

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PI Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
XX Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.
XX
PS Claim 31; SEQ ID NO 480; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
SQ Sequence 11 AA;
QY
Query Match 44.4%; Score 28; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 4 ERFPDENF 11
:::|||||
1 KKYPDLPNF 8
RESULT 27
ADC43422
ID ADC43422 standard; peptide; 11 AA.
XX
AC ADC43422;
XX
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 518.
XX
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.
XX
OS Variola virus.
XX
PN WO2003017943-A2.
XX
PD 06-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027066.
XX
PR 22-AUG-2001; 2001US-0314182P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is

PT useful for treating viral infections.
XX
XX Claim 31; SEQ ID NO 518; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
SQ Sequence 11 AA;
QY
Query Match 44.4%; Score 28; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 4 ERFPDENF 11
:::|||||
4 KKYPDLPNF 11
RESULT 28
ADC43411
ID ADC43411 standard; peptide; 12 AA.
XX
AC ADC43411;
XX
DT 18-DEC-2003 (first entry)
XX
DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 507.
XX
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.
XX
OS Variola virus.
XX
PN WO2003017943-A2.
XX
PD 06-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027066.
XX
PR 22-AUG-2001; 2001US-0314182P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
DR Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.
XX
PS Claim 31; SEQ ID NO 507; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where

CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11
ID ADC43385
DB 3 KKYPDINF 10

RESULT 29
ADC43385
ID ADC43385 standard; peptide; 12 AA.

AC ADC43385;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 481.

XX
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 481; 60pp; English.

XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein

CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFDPENF 11
ID ADC43423
DB 1 KKYPDINF 8

RESULT 30
ADC43423
ID ADC43423 standard; peptide; 12 AA.

AC ADC43423;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 519.

XX
KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 519; 60pp; English.

XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral

CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | | |
DB 4 KKYPD LNF 11

RESULT 31

ADC43434 standard; peptide; 12 AA.

XX
AC ADC43434;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 530.

XX
KW viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 530; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | | |
DB 5 KKYPD LNF 12

RESULT 32

ADC43398 standard; peptide; 12 AA.

XX
AC ADC43398;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 494.

XX
KW viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 494; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
:::| | | |

Db 2 KKYPDLNF 9

RESULT 33

ADCC4703
ID ADCC4703 standard; peptide; 12 AA.

AC ADCC4703;

DT 18-DEC-2003 (first entry)

DE Endothelial cell binding peptide SEQ ID NO:432.

KW endothelial cell binding protein; EGBP; anti-tumour; cytostatic;

KW vasotrophic; antipsoriatic; dermatological; ophthalmological;

KW antidiabetic; antiarthritic; vulnary; antidiabetic; antiinflammatory;

KW antibacterial; gynaecological; angiogenesis.

OS Synthetic.

PN WO2003037172-A2.

PD 08-MAY-2003.

PF 01-NOV-2002; 2002WO-US035258.

PR 01-NOV-2001; 2001US-0334822P.

PA (GPCB-) GPC BIOTECH INC.

PI Gyuris J, Lamphere L, Morris AJ, Tsaioun K;

DR WPI; 2003-482072/45.

Novel synthetic or recombinant polypeptide useful for promoting, reducing proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.

PS Claim 3; SEQ ID NO 432; 126pp; English.

The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell binding protein (EGBP) sequences. A peptide of the invention has anti-tumour, cytostatic, vasotrophic, antipsoriatic, dermatological, ophthalmological, antidiabetic, antiarthritic, vulnary, antidiabetic, antiinflammatory, antibacterial, and gynaecological activity. The peptide is useful for promoting, reducing the proliferation and/or migration of endothelial cells, by treating the cells with an EGBP agonist, which is preferably the peptide, to promote proliferation and/or migration of the treated cells, and for reducing or promoting angiogenesis, by treating the cells with an EGBP antagonist, which is preferably the peptide of the invention. A peptide of the invention is also useful for manufacturing a medicament for promoting angiogenesis, by admixing an EGBP agonist or EGBP antagonist to promote or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis. EGBP sequences are useful to alter the infectivity spectrum of a viral particle. The present sequence represents an EGBP of the invention.

SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGRFP 7
Db 3 VYGNRLP 9

RESULT 34

ADCC6084
ID ADCC6084 standard; peptide; 12 AA.

AC ADCC6084;

DT 18-DEC-2003 (first entry)

DE Chemokine binding peptide BKT-P125.

peptidic chemokine modulator; antiinflammatory; antiallergic; immunosuppressive; antidiabetic; antirheumatic; dermatological; antiarthritic; antibacterial; antipsoriatic; antiseborrheic; antiarteriosclerotic; hypotensive; neuroprotective; virucide; vasotrophic; cytostatic; inflammation; allergy; immune response; autoimmune reaction; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; allograft rejection; diabetes; sepsis; cancer; malignant cell growth; acne; infection; arthritis; colitis; psoriasis; atherosclerosis; hypertension; reperfusion ischaemia.

OS Synthetic.

PN WO2003072599-A2.

PD 04-SEP-2003.

PF 27-FEB-2003; 2003WO-IL000155.

PR 28-FEB-2002; 2002US-0359995P.

PA (BIOK-) BIOKINE THERAPEUTICS LTD.

PI Peled A, Eizenberg O, Vaizel-Ohayon D;

DR WPI; 2003-671869/63.

New peptidic chemokine modulator, useful for preparing a composition for treating a disease modulated through and/or caused by binding of a chemokine to a chemokine receptor, e.g., inflammation, diabetes, sepsis or cancer.

PS Example 1; Page 28; 43pp; English.

The present invention describes a peptidic chemokine modulator (I) for modulating a biological effect of a chemokine. (I) comprises a molecule consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr and Pro, and features at least 2 histidines spread along the molecule, where the molecule features an overall positive charge (family 1); or (b) the amino acids His, Pro, Thr, Leu, Arg and Trp and features at least two neighbouring histidines, where the molecule features an overall positive charge (family 2). Also described: (1) a composition for treating a condition involving abnormal cell migration in a subject; (2) a method for treating a disease modulated through and/or caused by binding of a chemokine to a chemokine receptor in a subject; (3) an antibody for binding to a chemokine-binding receptor that recognises at least a portion of a chemokine-binding receptor or the peptide; (4) a vaccine formed with the antibody; and (5) a method for producing an antibody. (I) has antiinflammatory, antiallergic, immunosuppressive, antidiabetic, antirheumatic, dermatological, antiarthritic, antibacterial, antipsoriatic, antiseborrheic, antiarteriosclerotic, hypotensive, neuroprotective, virucide, vasotrophic and cytostatic activities. The peptidic chemokine modulator is useful for preparing a composition for treating a disease modulated through and/or caused by binding of a chemokine to a chemokine receptor, comprising inflammation (primary or secondary), allergy, a non-optimal immune response, an autoimmune reaction (including rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and others), allograft rejection, diabetes, sepsis, cancer and any type of malignant cell growth, acne and chronic bacterial and viral infections, arthritis, colitis, psoriasis, atherosclerosis, hypertension or reperfusion ischaemia. The present sequence represents a chemokine binding peptide, which is used in an example from the present invention.

SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 7; Length 12;

Best Local Similarity 57.1%; Pred. NO. 4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IYGERFP 7
: ||| |
Db 3 VYGNRLP 9

RESULT 35

AAR46829

ID AAR46829 standard; protein; 13 AA.

AC AAR46829;

XX

DT 25-MAR-2003 (revised)

DT 19-AUG-1994 (first entry)

XX pH 2.5 acid phosphatase derived peptide #816:5Lpho.

XX pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid;

XX phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid;

XX plant; feed composition; filtration.

XX Synthetic.

XX WO9403612-A1.

XX 17-FEB-1994.

XX 30-JUL-1993; 93WO-FI000310.

XX 31-JUL-1992; 92US-00923724.

XX (ALKO-) ALKO LTD.

XX

PI Nevalainen HK, Palcheimo MT, Miettinen-Oinonen ASK, Torkkeli TK;

PI Cantrell M, Piddington C, Rambosek JA, Turunen MK, Fagerstroem RB;

XX WPI; 1994-065700/08.

XX Compsns. contg. phytate degrading enzymes - obt'd. by expression of their

PT genes in Trichoderma, used partic. for producing animal feed compns.

XX Example 4; Page 46; 142pp; English.

XX The sequences given in AAR46825-35 are peptides derived from the pH2.5

XX acid phosphatase protein. This phytase protein may be used in the

XX composition of the invention. The DNA encoding the phytase protein may be

XX introduced into a Trichoderma host which then expresses it and the

XX protein is collected from the culture medium. By using Trichoderma as a

XX host for Aspergillus phytate degrading enzymes such as this, a totally

XX different enzyme composition compared to that secreted from Aspergillus

XX results. The enzyme composition can be used for removal of phytic acid or

XX inositol hexaphosphoric acid from raw material, particularly plant

XX material. The composition is used in feed compositions for animals. By

XX using Trichoderma as a source of a composition containing phytase

XX degrading enzymes some difficult downstream processing problems, eg.

XX filtration, that occur with similar Aspergillus compositions are avoided

XX and yields are improved. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 13 AA;

Query Match 44.4%; Score 28; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. NO. 4.4e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGERFP 7
: ||| |

Db 2 HGERYP 7

RESULT 36
ADC43445

ID ADC43445 standard; peptide; 13 AA.

XX ADC43445;

XX 18-DEC-2003 (first entry)

XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 541.

XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;

XX herpes simplex virus; HSV; UL42 protein; variola virus A10L;

XX vaccinia virus virion core protein P4a;

XX human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;

XX viral budding; viral infectivity.

XX Variola virus.

XX WO2003017943-A2.

XX 06-MAR-2003.

XX 22-AUG-2002; 2002WO-US027066.

XX 22-AUG-2001; 2001US-0314182P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Morham S, Zavitz K, Hobden A;

XX WPI; 2003-371696/35.

XX Novel peptide, comprising a contiguous amino acid sequence of a viral

PT protein, capable of binding to a region of cellular protein AP-50 is

PT useful for treating viral infections.

XX Claim 31; SEQ ID NO 541; 60pp; English.

XX The invention relates to a novel isolated peptide comprising a contiguous

XX amino acid sequence of 7-30 amino acid residues of a viral protein, where

XX the contiguous amino acid sequence encompasses the YPXL motif of the

XX viral protein, and the 7-30 amino acid residues 121-435 of cellular

XX binding a region including the amino acid residues 121-435 of cellular

XX protein AP-50. The isolated 7-30 amino acid viral protein is selected

XX from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42

XX protein, variola virus A10L protein, vaccinia virus virion core protein

XX P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where

XX the contiguous amino acid sequence encompasses the YPXL motif of the viral

XX protein. The peptides of the invention are useful in the manufacture of a

XX medicament for treating viral infections caused by a virus selected from

XX HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting

XX viral budding from virus-infected cells and/or inhibiting viral

XX infectivity, thus inhibiting viral propagation in the cells. This

XX sequence represents a Variola smallpox virus A10L YPXL motif containing

XX peptide used in the treatment of viral infections of the invention.

SQ Sequence 13 AA;

Query Match 44.4%; Score 28; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. NO. 4.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERFPDENF 11
: : ||| |

Db 6 KKYPDLNF 13

RESULT 37

ID ADC43424 standard; peptide; 13 AA.

XX ADC43424;

DT 18-DEC-2003 (first entry)

XX

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 520.
XX
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

OS Variola virus.
XX
XX WO2003017943-A2.

XX
XX 06-MAR-2003.

XX
XX 22-AUG-2002; 2002WO-US027066.

XX
XX 22-AUG-2001; 2001US-0314182P.

XX
XX (MYRI-) MYRIAD GENETICS INC.

XX
XX Morham S, Zavitz K, Hobden A;

XX
XX WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 520; 60pp; English.

XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 13 AA;

Query Match 44.4%; Score 28; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERPPDENF 11
:::| | |
DB 4 KKYPDLNF 11

RESULT 38
ADC43399
ID ADC43399 standard; peptide; 13 AA.

XX
XX ADC43399;

XX
XX 18-DEC-2003 (first entry)

XX
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 495.

XX
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;

KW viral budding; viral infectivity.

XX
XX Variola virus.

XX
XX WO2003017943-A2.

XX
XX 06-MAR-2003.

XX
XX 22-AUG-2002; 2002WO-US027066.

XX
XX 22-AUG-2001; 2001US-0314182P.

XX
XX (MYRI-) MYRIAD GENETICS INC.

XX
XX Morham S, Zavitz K, Hobden A;

XX
XX WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 495; 60pp; English.

XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 13 AA;

Query Match 44.4%; Score 28; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERPPDENF 11
:::| | |
DB 2 KKYPDLNF 9

RESULT 39
ADC43412
ID ADC43412 standard; peptide; 13 AA.

XX
XX ADC43412;

XX
XX 18-DEC-2003 (first entry)

XX
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 508.

XX
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

XX
XX Variola virus.

XX
XX WO2003017943-A2.

```
PD 06-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027066.
XX
XX 22-AUG-2001; 2001US-0314182P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
XX Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.
XX
XX Claim 31; SEQ ID NO 508; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompass the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 44.4%; Score 28; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 ERFDPDEF 11
Db 3 KKYPDLNF 10
RESULT 40
ADCC43435
ID ADC43435 standard; peptide; 13 AA.
XX
XX ADC43435;
AC
XX 18-DEC-2003 (first entry)
DT
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 531.
DE
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.
XX
XX Variola virus.
OS
XX WO2003017943-A2.
PN
XX 06-MAR-2003.
PD
XX 22-AUG-2002; 2002WO-US027066.
PF
XX 22-AUG-2001; 2001US-0314182P.
PR
XX
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PA (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-371696/35.
XX
XX Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.
XX
XX Claim 31; SEQ ID NO 531; 60pp; English.
XX
XX The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompass the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 44.4%; Score 28; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 ERFDPDEF 11
Db 5 KKYPDLNF 12
RESULT 41
ADCC43386
ID ADC43386 standard; peptide; 13 AA.
XX
XX ADC43386;
AC
XX 18-DEC-2003 (first entry)
DT
XX Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 482.
DE
XX viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.
XX
XX Variola virus.
OS
XX WO2003017943-A2.
PN
XX 06-MAR-2003.
PD
XX 22-AUG-2002; 2002WO-US027066.
PF
XX 22-AUG-2001; 2001US-0314182P.
PR
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX Morham S, Zavitz K, Hobden A;
PI
XX WPI; 2003-371696/35.
DR
XX
```

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 482; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, varicella virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and varicella virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

SQ Sequence 13 AA;

Query Match 44.4%; Score 28; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDPENF 11
:::| | |
Db 1 KKYPDLNF 8

RESULT 42
ADC43436

ID ADC43436 standard; peptide; 14 AA.

AC ADC43436;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 532.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; varicella virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 532; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polypeptide, herpes simplex virus (HSV) UL42
CC protein, varicella virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and varicella virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

SQ Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 ERPDPENF 11
:::| | |
Db 5 KKYPDLNF 12

RESULT 43
ADC43387

ID ADC43387 standard; peptide; 14 AA.

AC ADC43387;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID NO 483.

KM viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KM herpes simplex virus; HSV; UL42 protein; varicella virus A10L;
KM vaccinia virus virion core protein P4a;
KM human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KM viral budding; viral infectivity.

OS Variola virus.

PN WO2003017943-A2.

PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

DR WPI; 2003-371696/35.

PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

PS Claim 31; SEQ ID NO 483; 60pp; English.

CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected

CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPDENF 11
::|||
Db 1 KKYPDLNF 8

RESULT 44

ADC43413
ID ADC43413 standard; peptide; 14 AA.

XX
AC ADC43413;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 509.

XX
KW viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

OS Variola virus.

XX
PN WO2003017943-A2.

XX
PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

XX
PA (MYRI-) MYRIAD GENETICS INC.

XX
PI Morham S, Zavitz K, Hobden A;

XX
DR WPI; 2003-371696/35.

XX
PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

XX
PS Claim 31; SEQ ID NO 509; 60bp; English.

XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from

CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

XX
SQ Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 ERFPDENF 11
::|||
Db 3 KKYPDLNF 10

RESULT 45

ADC43425
ID ADC43425 standard; peptide; 14 AA.

XX
AC ADC43425;

DT 18-DEC-2003 (first entry)

DE Variola smallpox virus A10L YPXL motif containing peptide, SEQ ID No 521.

XX
KW viral; YPXL; cellular protein AP-50; hepatitis C virus; HCV;
KW herpes simplex virus; HSV; UL42 protein; variola virus A10L;
KW vaccinia virus virion core protein P4a;
KW human parainfluenza virus haemagglutinin-neuraminidase; HSP-1;
KW viral budding; viral infectivity.

OS Variola virus.

XX
PN WO2003017943-A2.

XX
PD 06-MAR-2003.

PF 22-AUG-2002; 2002WO-US027066.

PR 22-AUG-2001; 2001US-0314182P.

XX
PA (MYRI-) MYRIAD GENETICS INC.

XX
PI Morham S, Zavitz K, Hobden A;

XX
DR WPI; 2003-371696/35.

XX
PT Novel peptide, comprising a contiguous amino acid sequence of a viral
PT protein, capable of binding to a region of cellular protein AP-50 is
PT useful for treating viral infections.

XX
PS Claim 31; SEQ ID NO 521; 60bp; English.

XX
CC The invention relates to a novel isolated peptide comprising a contiguous
CC amino acid sequence of 7-30 amino acid residues of a viral protein, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the
CC viral protein, and the 7-30 amino acid viral protein is capable of
CC binding a region including the amino acid residues 121-435 of cellular
CC protein AP-50. The isolated 7-30 amino acid viral protein is selected
CC from hepatitis C virus (HCV) polyprotein, herpes simplex virus (HSV) UL42
CC protein, variola virus A10L protein, vaccinia virus virion core protein
CC P4a, and human parainfluenza virus haemagglutinin-neuraminidase, where
CC the contiguous amino acid sequence encompasses the YPXL motif of the viral
CC protein. The peptides of the invention are useful in the manufacture of a
CC medicament for treating viral infections caused by a virus selected from
CC HCV, HSP-1 and variola virus. The peptides are also useful for inhibiting
CC viral budding from virus-infected cells and/or inhibiting viral
CC infectivity, thus inhibiting viral propagation in the cells. This
CC sequence represents a Variola smallpox virus A10L YPXL motif containing
CC peptide used in the treatment of viral infections of the invention.

SO Sequence 14 AA;

Query Match 44.4%; Score 28; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 4 ERFPDENF 11
:::| |
Db 4 KKYPDLNF 11

Search completed: August 30, 2004, 10:49:33
Job time : 18.3885 secs

QY 1 RFPDEF 7
|||:
Db 2 RFPDEF 8

RESULT 2

ID P96352 PRELIMINARY; PRT; 10 AA.
AC P96352;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAY-1997 (TREMBlrel. 16, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
OX NCBI_TaxID=2743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49840;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68077; AAB48027.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
|||:
Db 3 DENYAL 8

RESULT 3

ID Q93LE5 PRELIMINARY; PRT; 10 AA.
AC Q93LE5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213;
RA Williams K.P.;
RT "The tmRNA website.";
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RT "Phylogenetic analysis of tmRNA.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040837; AAK83525.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
|||:
Db 3 DENYAL 8

RESULT 4
ID P96321 PRELIMINARY; PRT; 10 AA.
AC P96321;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023883; PubMed=7524073;
RA Komine Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from
RT Escherichia coli.";
RN Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68074; AAB48024.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
|||:
Db 3 DENYAL 8

RESULT 5

ID P96306 PRELIMINARY; PRT; 10 AA.
AC P96306;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33658;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68075; AAB48022.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 46.0%; Score 23; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
|||:
Db 3 DENYAL 8

RESULT 6


```
P96350
ID P96350 PRELIMINARY; PRT; 14 AA.
AC P96350;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68079; AAB48026.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1349 MW; CE5F7318D3BE7D7D CRC64;

Query Match 46.0%; Score 23; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7
Db 3 DENF 6

RESULT 7
P96305 PRELIMINARY; PRT; 10 AA.
ID P96305;
AC P96305;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Alteromonas haloplanktis (Pseudalteromonas haloplanktis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Pseudalteromonas.
OX NCBI_TaxID=228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14393;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68076; AAB48021.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1053 MW; 857BD235AB544AAA CRC64;

Query Match 42.0%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
Db 3 DDNYSL 8

RESULT 8
P96423 PRELIMINARY; PRT; 10 AA.
ID P96423;
AC P96423;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Coded portion of proteolysis tag (Translated portion of tmRNA gene
DE ssaA) (Fragment).
GN PA0826.1.
```

```
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25330;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; U68078; AAB48029.1; -.
DR EMBL; AE004517; AA042616.1; -.
KW Complete proteome.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1037 MW; 857BD22DCB544AAA CRC64;

Query Match 40.0%; Score 20; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
Db 3 DDNYAL 8

RESULT 9
Q8WY56 PRELIMINARY; PRT; 13 AA.
ID Q8WY56;
AC Q8WY56;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Epithelial sodium channel beta-3 subunit (Fragment).
GN SCN1B.
OS Homo sapiens (Human).
OC Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;
RT "Genomic organization of the 5' end of human beta ENaC and preliminary
RT characterization of its promoter.";
RL Am. J. Physiol. Renal Physiol. 0:0-0(2002).
DR EMBL; AF260228; AAL48197.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;

Query Match 40.0%; Score 20; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFK 8
Db 9 DKNFQ 13
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```
RESULT 10
ID Q45876 PRELIMINARY; PRT; 14 AA.
AC Q45876;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HA-II protein (Fragment).
GN HA-II.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 7273;
RA East A.K., Stacey J.M., Collins M.D.;
RT "Cloning and sequencing of a hemagglutinin component of the botulinum
neurotoxin complex encoded by Clostridium botulinum types A and B.";
RL Syst. Appl. Microbiol. 17:306-312(1994).
DR EMBL; X79102; CAAS5711.1; -.
DR PIR; S58866; S58866.
DR InterPro; IPR008903; Botulinum_HA-17.
DR Pfam; PF05588; botulinum_HA-17; 1.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1628 MW; CD689B0937D75E29 CRC64;

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
|:|:|
Db 9 PNGNYK 14

RESULT 11
ID Q45872 PRELIMINARY; PRT; 14 AA.
AC Q45872; Q45869;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE (NCTC 7272 type A) HA-33 and P-21 genes (Fragment).
GN HA-II.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 7272, TYPE A, and 17B;
RA East A.K., Stacey J.M., Collins M.D.;
RL Syst. Appl. Microbiol. 17:306-312(1994).
DR EMBL; X79104; CAAS5719.1; -.
DR PIR; S58862; S58862.
DR InterPro; IPR008903; Botulinum_HA-17.
DR Pfam; PF05588; botulinum_HA-17; 1.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1656 MW; CD689B1B3CD75E29 CRC64;

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
|:|:|
Db 9 PNGNYK 14

RESULT 12
Q9UCRO
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```
ID Q9UCRO PRELIMINARY; PRT; 10 AA.
AC Q9UCRO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Diotta L.A.;
RT "Identification, purification, and partial sequence analysis of
autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0030334; P:regulation of cell migration; IDA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;

Query Match
Best Local Similarity 38.0%; Score 19; DB 4; Length 10;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENFKL 9
|:|:|
Db 3 PFENINL 9

RESULT 13
ID Q7ZSA2 PRELIMINARY; PRT; 10 AA.
AC Q7ZSA2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Fraisi P., Forss-Petter S., Berger J.;
RT "A novel relative of Bubblegum.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ57571; CAE12153.1; -.
KW Hypothetical protein.
SQ SEQUENCE 10 AA; 1086 MW; 622094D8786769D4 CRC64;

Query Match
Best Local Similarity 36.0%; Score 18; DB 4; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3
|:|:|
Db 3 RFP 5

RESULT 14
ID Q9QVF7 PRELIMINARY; PRT; 10 AA.
AC Q9QVF7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).
OS Rattus sp.
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92135065; PubMed=1777418;
 RA Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
 RA Yasuda T., Koike T.;
 RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
 RT cDNA cloning and inter-species differences of beta 2-GPI in
 RT alternation of anticardiolipin binding.";
 RL Int. Immunol. 3:1217-1221(1991).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1100 MW; 94E681B767376EA1 CRC64;

Query Match 36.0%; Score 18; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PDE 5
 |||
 Db 7 PDE 9

RESULT 15

O63389 PRELIMINARY; PRT; 10 AA.
 ID Q63389
 AC Q63389;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Ornithine decarboxylase (ODC).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=89255378; PubMed=2722815;
 RA Wen L., Huang J.K., Blackshear P.J.;
 RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential
 RT regulatory elements, and comparison to the mouse gene.";
 RL J. Biol. Chem. 264:9016-9021(1989).
 DR EMBL; J04791; AAA66163.1; -.
 DR PIR; B33710; B33710.
 SQ SEQUENCE 10 AA; 1074 MW; 30F6EE69D415BDC7 CRC64;

Query Match 36.0%; Score 18; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFP 3
 |||
 Db 6 RFP 8

RESULT 16

O9DZ32 PRELIMINARY; PRT; 11 AA.
 ID Q9DZ32
 AC Q9DZ32;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Gag polypeptide (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20461476; PubMed=11005867;

RA Martinez-Picado J., Depasquale M.P., Kartsonis N., Hanna G.J.,
 RA Wong J., Finzi D., Rosenberg E., Guntard H.F., Sutton L., Savara A.,
 RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
 RA Siliciano R., D'Aquila R.T.;
 RT "Antiretroviral resistance during successful therapy of HIV type 1
 RT infection.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
 DR EMBL; AF292799; AAG25407.1; -.
 KW Polypeptide.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 36.0%; Score 18; DB 15; Length 11;
 Best Local Similarity 37.5%; Pred. No. 1e+04;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RFPDENFK 8
 |||:|:
 Db 4 RTPNERLR 11

RESULT 17

O9UNV6 PRELIMINARY; PRT; 13 AA.
 ID Q9UNV6
 AC Q9UNV6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Inosine monophosphatase 2 (Fragment).
 GN IMPA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97463449; PubMed=9322233;
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
 RA Detera-Wadleigh S.D.;
 RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
 RT susceptibility region for bipolar disorder.";
 RL Mol. Psychiatry 2:393-397(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20284187;
 RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
 RA Esterling L.E., Detera-Wadleigh S.D.;
 RT "Genomic structure and novel variants of myo-inositol monophosphatase
 RT 2.";
 RL Mol. Psychiatry 5:165-171(2000).
 DR EMBL; AF085628; AAD22141.1; -.
 DR EMBL; AF085627; AAD22141.1; JOINED.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 36.0%; Score 18; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFP 3
 |||
 Db 7 RFP 9

RESULT 18

O52840 PRELIMINARY; PRT; 14 AA.
 ID O52840
 AC O52840;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Homology with C-terminus of other Rhizobium nodB genes.

OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97002748; PubMed=8850088;
RA Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,
RA Rockman E.S., Lewis P.E., Pankhurst C.E.;
RT "Novel and complex chromosomal arrangement of Rhizobium loti
modulation genes."
RT Mol. Plant Microbe Interact. 9:187-197(1996).
RL EMBL: L06241; AAB47352.1; -.
DR EMBL: L06241; AAB47352.1; -.
SQ SEQUENCE 14 AA; 1600 MW; 90C26EC32C8F34C5 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3
DB 9 RFP 11

RESULT 19
ID Q52636 PRELIMINARY; PRT; 14 AA.
AC Q52636;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tral. protein (Fragment).
GN TRAL.
OS Escherichia coli.
OG Plasmid R124.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86059219; PubMed=2999074;
RA Frost L.S., Finlay B.B., Opgenorth A., Paranchych W., Lee J.S.;
RT "Characterization and sequence analysis of pilin from F-like
plasmids."
RL J. Bacteriol. 164:1238-1247(1985).
DR EMBL: K03092; AAA92759.1; -.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
KM Plasmid.
FT NON TER
SQ SEQUENCE 14 AA; 1713 MW; 5CCA91188EB30E23 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3
DB 12 RFP 14

RESULT 20
ID Q7X139 PRELIMINARY; PRT; 8 AA.
AC Q7X139;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SecE (Fragment).
OS Staphylococcus cohnii.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=29382;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=GITU9122;
RA Morikawa K., Inose Y., Ohta T.;
RT "A new Staphylococcal sigma factor in the conserved gene cassette:
RT Functional significance and implication for the evolutionary
RT processes."
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY234840; AA062607.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 1014 MW; F0C9C44B13333DD6 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENF 7
DB 5 ENF 7

RESULT 21
ID P96421 PRELIMINARY; PRT; 10 AA.
AC P96421;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19424;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL: U68080; AAB48028.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1038 MW; 857BD22DCB41AB1A CRC64;

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DENFKL 9
DB 3 DETYAL 8

RESULT 22
ID Q9A1Z8 PRELIMINARY; PRT; 11 AA.
AC Q9A1Z8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbott P., Brennan E.B., Burckhardt D.H.,
BAumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts."
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont."
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211126; AAK15376.1; -
DR GO; GO:0004812; F:trna ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1384 MW; 07A038324339C724 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ENFKL 9
Db 7 KNFNL 11

RESULT 23

Q9TWV4 PRELIMINARY; PRT; 12 AA.
AC Q9TWV4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Light yellow cell peptide (Fragment).
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RX MEDLINE=93095719; PubMed=1334202;
RA Hoek R.M., Li K.W., van Minnen J., Geraerts W.P.;
RT "Chemical characterization of a novel peptide from the neuroendocrine
RT light yellow cells of Lymnaea stagnalis."
RL Brain Res. Mol. Brain Res. 16:71-74(1992).
DR PIR; A56878; A56878.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1385 MW; 44255417732045B3 CRC64;

Query Match 34.0%; Score 17; DB 5; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.7e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
Db 3 PDKSILL 9

RESULT 24

Q9RSR5 PRELIMINARY; PRT; 14 AA.
AC Q9RSR5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 25-kDa elastin-binding protein (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE.
RX MEDLINE=92078218; PubMed=1744133;
RA Park P.W., Roberts D.D., Grosso L.E., Parks W.C., Rosenbloom J.,
RA Abrams W.R., Mecham R.P.;
RT "Binding of elastin to Staphylococcus aureus."
RL J. Biol. Chem. 266:23399-23406(1991).
DR PIR; A41589; A41589.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 34.0%; Score 17; DB 11; Length 14;
Best Local Similarity 75.0%; Pred. No. 2e+04;

SQ SEQUENCE 14 AA; 1754 MW; 96CA3586E99D1CCA CRC64;

Query Match 34.0%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NFK 8
Db 3 NFK 5

RESULT 25

P78359 PRELIMINARY; PRT; 14 AA.
AC P78359;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NF-kappa-B transcription factor p65 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUE=Umbilical vein;
RA Remacle J.E., Brys R., Pype S., Nelles L., Huylebreeck D.;
RT "5' cDNA sequence RelA isolated from Human umbilical vein endothelial
RT cells."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88316; AAB48487.1; -
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 34.0%; Score 17; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. No. 2e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DENFKL 9
Db 2 DELFPL 7

RESULT 26

Q9JUT5 PRELIMINARY; PRT; 14 AA.
AC Q9JUT5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE B-Raf protein (Fragment).
GN B-RAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Barnier J.V.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Barnier J.V., Papin C., Bychene A., Iecocq O.;
RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-
RT specific expression."
RL J. Biochem. 270:23381-23389(1995).
DR EMBL; AJ276308; CAB81556.1; -
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 34.0%; Score 17; DB 11; Length 14;
Best Local Similarity 75.0%; Pred. No. 2e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENE 7
| |
Db 1 DEXF 4

RESULT 27

Q93LE4 PRELIMINARY; PRT; 9 AA.
AC Q93LE4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OS Proteolysis tag (Fragment).
OC Helicobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213;
RA Williams K.P.;
RT "The tmRNA website."
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RT "Phylogenetic analysis of tmRNA."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040838; AAK83526.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 937 MW; 7CDBD72DCB544AAB CRC64;

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENEKL 9
: : :
Db 2 EDNYAL 7

RESULT 28

Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REase.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T.; Bourne J.C.; Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
modification systems."
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.4e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6
| | |

Db 4 PDLN 7

RESULT 29

Q81VH0 PRELIMINARY; PRT; 12 AA.
AC Q81VH0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Truncated PAX6 protein (Fragment).
GN PAX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Neethirajan G.; Krishnadas S.R.; Vijayalakshmi P.; Sundaresan P.;
RT "Mutation analysis in Human PAX6 gene of Aniridia."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548390; AAN86817.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1511 MW; 9E169541A67B51F1 CRC64;

Query Match 32.0%; Score 16; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
: : :
Db 7 YPD 9

RESULT 30

Q88577 PRELIMINARY; PRT; 12 AA.
AC Q88577;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TO(4);
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E.; Calenoff M.A.; Simpson S.; Jensen K.; Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80885; AAA73156.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
: : :
Db 7 YPD 9

RESULT 31

Q88578 PRELIMINARY; PRT; 12 AA.
AC Q88578;
DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OC NCBI_TaxID=12124;
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO(B15);
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80886; AAA73157.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FPD 4
Db 7 YPD 9

RESULT 32

Q88579 PRELIMINARY; PRT; 12 AA.
ID Q88579
AC Q88579;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OC NCBI_TaxID=12124;
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VL;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80887; AAA73158.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FPD 4
Db 7 YPD 9

RESULT 33

Q88575 PRELIMINARY; PRT; 12 AA.
ID Q88575
AC Q88575;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OC NCBI_TaxID=12124;
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80883; AAA73154.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FPD 4
Db 7 YPD 9

RESULT 34

Q88580 PRELIMINARY; PRT; 12 AA.
ID Q88580
AC Q88580;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OC NCBI_TaxID=12124;
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vilyuisk;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80888; AAA73159.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FPD 4
Db 7 YPD 9

RESULT 35

Q88582 PRELIMINARY; PRT; 12 AA.
ID Q88582
AC Q88582;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OC NCBI_TaxID=12124;
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=TO(Yale);
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence";
RL J. Virol. 66:1951-1958(1992).
DR EMBL: M80890; AAA73161.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 12; Length 12;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
DB 7 YPD 9

RESULT 36
Q88581 PRELIMINARY; PRT; 12 AA.
AC Q88581;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence";
RL J. Virol. 66:1951-1958(1992).
DR EMBL: M80889; AAA73160.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 12; Length 12;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
DB 7 YPD 9

RESULT 37
Q88576 PRELIMINARY; PRT; 12 AA.
AC Q88576;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence";

RL J. Virol. 66:1951-1958(1992).
DR EMBL: M80884; AAA73155.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 12; Length 12;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
DB 7 YPD 9

RESULT 38
Q865C9 PRELIMINARY; PRT; 13 AA.
AC Q865C9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Glutamine synthetase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Vallet J.L., Christenson R.K.;
RT "Characterization of porcine glutamine synthetase";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY216477; AA064254.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 6; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFR 8
DB 6 DEPFQ 10

RESULT 39
Q8SL68 PRELIMINARY; PRT; 13 AA.
AC Q8SL68;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PsbA (Fragment).
GN PsbA.
OS Monanthus anagensis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Monanthus.
OX NCBI_TaxID=91110;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
Crassulaceae";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY082189; AAM13933.1; -.
DR GO: 0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
SQ SEQUENCE 13 AA; 1361 MW; C0FB1B6DAD15CB02 CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 8; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDEN 6
Db 8 FPSIN 12

RESULT 40

Q83171 PRELIMINARY; PRT; 13 AA.
AC Q83171;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Cauliflower mosaic virus.
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OX NCBI_TaxID=10641;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8155790; PubMed=2894473;
RA Penswick J., Hubler R., Hohn T.;
RT "A viable mutation in cauliflower mosaic virus, a retroviruslike plant virus, separates its capsid protein and polymerase genes."
RL J. Virol. 62:1460-1463(1988).
DR EMBL; M19741; AAA66605.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1600 MW; 5DD9E7FDCA45CB13 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFK 8
Db 4 PMKEFK 9

RESULT 41

Q8J32 PRELIMINARY; PRT; 13 AA.
AC Q8J32;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE 37LRP/p40 (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with limited available sequence information: high nucleotide diversity revealed in the avian genome."
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454232; AAM22911.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;

Query Match 32.0%; Score 16; DB 13; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDE 5
Db 9 RDPDE 13

RESULT 42

Q55326 PRELIMINARY; PRT; 14 AA.
AC Q55326;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative ORF1 (Fragment).
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR6;
RX MEDLINE=92201692; PubMed=1551590;
RA Rhel E., Stirewalt V.L., Gasparich G.E., Bryant D.A.;
RT "The psac genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning and sequence analysis."
RL Gene 112:123-128(1992).
DR EMBL; M86238; AAA27351.1; -.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;

Query Match 32.0%; Score 16; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.1e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ENFKL 9
Db 2 KGFKL 6

RESULT 43

Q8V3U6 PRELIMINARY; PRT; 14 AA.
AC Q8V3U6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Tomato yellow leaf curl virus TYLCV/TYLCV recombinant isolate Spain ES42199 C1 (Fragment).
DE ES42199 C1 (Fragment).
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYLCV/TYLCV recombinant isolate Spain ES42199;
RA Monci F., Navas-Castillo J., Moriones E.;
RT "Evidence of the occurrence of a natural recombinant between Tomato yellow leaf curl virus."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401478; AAL59158.1; -.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1710 MW; D296A16BF41A7FD9 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 14;
Best Local Similarity 28.6%; Pred. No. 3.1e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
Db 3 PKRFQI 9

RESULT 44

P72279 PRELIMINARY; PRT; 8 AA.
AC P72279;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Biphenyl dioxygenase (Fragment).

GN BPHB.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz E., Timmis K.N.;
RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
RT positive bacterium Rhodococcus globerulus P6 to multicomponent
RT dioxygenases of gram-negative bacteria.";
RL Gene 156:11-18(1995).
DR EMBL; X80041; CAA56350.1;
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
KW Dioxygenase.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RFPDE 5
Db 2 RLQDE 6

RESULT 45

Q7T282 PRELIMINARY; PRT; 8 AA.
ID Q7T282;
AC Q7T282;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Calmodulin (Fragment).
OS Geochelone nigra (Galapagos giant tortoise).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Testudinidae; Geochelone.
OX NCBI_TaxID=66189;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ESP1;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101722; AAM47127.1; .
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 892 MW; SD0769CAA041A874 CRC64;

Query Match 30.0%; Score 15; DB 13; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
Db 6 FPE 8

Search completed: August 30, 2004, 10:55:26
Job time : 10.6655 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.55068 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-7
Perfect score: 50
Sequence: 1 RFPDENFKL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	46.0	11	1	TKN4_PSEGU P42989 pseudophryn
2	21	42.0	12	1	FIF1_SARBU P83349 sarcophaga
3	20	40.0	11	1	EFG_GLOPA P81350 clostridium
4	20	40.0	14	1	LPER_BACLI Q04303 bacillus li
5	19	38.0	8	1	FAR2_MACRS P83275 macrobrachi
6	19	38.0	9	1	FAR3_MACRS P83276 macrobrachi
7	19	38.0	10	1	FAR7_MACRS P83280 macrobrachi
8	19	38.0	10	1	SLAP_BACTG P49325 cydia pomon
9	18	36.0	8	1	ALU1_CYPDO P82152 cydia pomon
10	18	36.0	8	1	FAR1_PENMO P83316 penaeus mon
11	18	36.0	8	1	FAR3_HOMAM P41486 homarus ame
12	18	36.0	8	1	UC26_MAIZE P80632 zea mays (m
13	18	36.0	9	1	UPA3_HUMAN P30089 homo sapien
14	18	36.0	11	1	TKN1_PSEGU P42986 pseudophryn
15	18	36.0	11	1	TKN1_UPERU P08612 uperoleia r
16	18	36.0	11	1	TKN2_PSEGU P42987 pseudophryn
17	18	36.0	11	1	TKN5_PSEGU P42990 pseudophryn
18	18	36.0	14	1	MARI_ALTPS P29399 alteromonas
19	17	34.0	8	1	FAR1_PANRE P41872 panagrellus
20	17	34.0	9	1	FAR2_PANRE P41873 panagrellus
21	17	34.0	9	1	FAR4_CALVO P41859 calliphora
22	17	34.0	10	1	URAT_HUMAN P34990 homo sapien
23	17	34.0	10	1	UXA6_CHLTR P38007 chlamydia t
24	17	34.0	11	1	COXA_CANFA P99501 canis fami1
25	17	34.0	14	1	UC04_MAIZE P80610 zea mays (m
26	16	32.0	9	1	FAR1_CALVO P41856 calliphora
27	16	32.0	9	1	FAR2_CALVO P41857 calliphora
28	16	32.0	9	1	FAR3_CALVO P41858 calliphora
29	16	32.0	9	1	FAR1_GARBU P83350 sarcophaga
30	16	32.0	10	1	PORB_METTM P80901 methanobact
31	16	32.0	10	1	PPCK_FASHE P80525 fasciola he
32	16	32.0	13	1	MPI_MICOC P81532 microplitis
33	16	32.0	14	1	ATP6_SPIOLO P80086 spiniacia ol

34	15	30.0	8	1	ALL6_CYPDO P82157 cydia pomon
35	15	30.0	9	1	FAR5_CALVO P41860 calliphora
36	15	30.0	9	1	FARA_CALVO P41865 calliphora
37	15	30.0	10	1	Q2OB_COMTE P80465 comamonas t
38	15	30.0	10	1	UPA2_HUMAN P30088 homo sapien
39	15	30.0	11	1	TKNA_RANCA P22688 rana catesb
40	15	30.0	12	1	FARI_CALVO P41869 calliphora
41	15	30.0	12	1	TKN1_KASMA P08613 kassina mac
42	15	30.0	13	1	ADFB_TEMMO P83109 tenebrio mo
43	15	30.0	13	1	LPAA_PORGI P81411 porphyromon
44	14	28.0	8	1	LCK3_LEUMA P21142 leucophaea
45	14	28.0	9	1	SAMP_MUSCA P19095 mustelus ca

ALIGNMENTS

```
RESULT 1
TKN4_PSEGU
ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide 1 (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
CX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 46.0%; Score 23; DB 1; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
Db 4 PDEFFGL 10

RESULT 2
FIF1_SARBU
ID FIF1_SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FIRFamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Sarcophagidae; Sarcophaga.
 OC NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 RC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438685;
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
 RT "Identification in *Drosophila melanogaster* of the invertebrate G
 RT protein-coupled FMRFamide receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
 CC junctions.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 12 12
 FT SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;
 SQ

Query Match 42.0%; Score 21; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
 DB 5 PSDNF 9

RESULT 3
 EFG_CLOPA STANDARD; PRT; 11 AA.
 ID EFG_CLOPA
 AC P81350;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (CP 5) (Fragment).
 GN FUSA.
 OS Clostridium pasteurianum.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 OC NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from *Clostridium pasteurianum* W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
 DR InterPro: IPR000795; EF_GTPbind.
 DR PROSITE: PS00301; EFATOR_GTP; PARTIAL.
 KW Elongation factor; Protein biosynthesis; GTP-binding.
 FT NON_TER 11 11
 FT SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;
 SQ

Query Match 40.0%; Score 20; DB 1; Length 11;
 Best Local Similarity 37.5%; Pred. No. 4.3e+02;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RFPDENFX 8
 DB 1 RFPDENFX 8

DB 1 KYPLEKFX 8

RESULT 4
 LPER_BACLI STANDARD; PRT; 14 AA.
 ID LPER_BACLI
 AC Q04303;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Brythromycin resistance leader peptide (23S rRNA methylase leader
 DE peptide).
 OS Bacillus licheniformis, and
 OS Bacillus anthracis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1402, 1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.licheniformis; STRAIN=EMF-1;
 RX MEDLINE=84245158; PubMed=6429477;
 RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;
 RT "DNA sequence and regulation of ermB, a macrolide-lincosamide-
 RT streptogramin B resistance element from *Bacillus licheniformis*.";
 RL Mol. Gen. Genet. 194:349-356(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.licheniformis; STRAIN=EMF-1;
 RX MEDLINE=91310580; PubMed=1713206;
 RA Kwak J.-K., Choi E.-C., Weisblum B.;
 RT "Transcriptional attenuation control of ermK, a
 RT macrolide-lincosamide-streptogramin B resistance determinant from
 RT *Bacillus licheniformis*.";
 RL J. Bacteriol. 173:4725-4735(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.anthraxis; STRAIN=590;
 RX MEDLINE=93232776; PubMed=8473865;
 RA Kim H.-S., Choi E.-C., Kim B.-K.;
 RT "A macrolide-lincosamide-streptogramin B resistance determinant from
 RT *Bacillus anthracis* 590: cloning and expression of ermJ.";
 RL J. Gen. Microbiol. 139:601-607(1993).
 CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF
 CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B
 CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L08389; AAA22596.1; -.
 DR EMBL: M29832; AAA22598.1; -.
 DR PIR: A42473; A42473.
 KW Antibiotic resistance; leader peptide.
 FT SEQUENCE 14 AA; 1732 MW; 5D1138B59F32ED07 CRC64;
 SQ

Query Match 40.0%; Score 20; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RFPDEN 6
 DB 8 RFPDEN 13

RESULT 5
 FAR2_MACRS STANDARD; PRT; 8 AA.
 ID FAR2_MACRS
 AC P83275;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLIP2 (ADKMFILF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonidae; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigornkul P., Sarathongkum W., Jaideechoey S., Longyant S.,
RA Sithigornkul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
freshwater prawn Macrobrachium rosenbergii."
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 38.0%; Score 19; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7
Db 2 DKNF 5

RESULT 6
FAR7_MACRS
ID FAR7_MACRS STANDARD; PRT; 9 AA.
AC P83276;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLIP3 (NYDKMFLF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonidae; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigornkul P., Sarathongkum W., Jaideechoey S., Longyant S.,
RA Sithigornkul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
freshwater prawn Macrobrachium rosenbergii."
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;

Query Match 38.0%; Score 19; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7
Db 3 DKNF 6

RESULT 7
FAR7_MACRS

ID FAR7_MACRS STANDARD; PRT; 10 AA.
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLIP7 (GYGDRNFLF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonidae; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigornkul P., Sarathongkum W., Longyant S., Panchan N.,
RA Sithigornkul W., Petsom A.;
RT "Three more novel neuropeptide-like neuropeptide sequences from the
eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match 38.0%; Score 19; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENF 7
Db 2 YGDRNF 7

RESULT 8
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=9007811; PubMed=2592346;
RA Luckeich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis."
J. Bacteriol. 171:6656-6667(1989).
CC -1- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
of proteins which coat the surface of bacteria.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 38.0%; Score 19; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
Db 5 FPD 7

RESULT 9

ALLI_CYDPO STANDARD; PRT; 8 AA.
ID P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydastatin 1.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RT "Lepidopteran peptides of the allostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 DENF 9
DB 2 DRNF 8

RESULT 10

FAR1_PENMO STANDARD; PRT; 8 AA.
ID FAR1_PENMO
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLR1 (GDRNFRF-amide).
OS Pennaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Pennaeidea;
OC Pennaeidae; Pennaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RT Chaivithangskura P., Sithigorngul W., Patsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Pennaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7
DB 2 DRNF 5

RESULT 11

FAR3_HOMAM STANDARD; PRT; 8 AA.
ID FAR3_HOMAM
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide 3 (FLR 3) (F2).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=8816164; PubMed=3429714;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRamide-like immunoreactive
substances from the lobster nervous system: isolation and sequence
analysis of two closely related peptides."
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 mM
potassium in the presence of calcium.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7
DB 2 DRNF 5

RESULT 12

UC26_MAIZE STANDARD; PRT; 8 AA.
ID UC26_MAIZE
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
(Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RT Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 7.0, its MW is: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 36.0%; Score 18; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFK 8
| : ||
Db 3 PRDQFK 8

RESULT 13

UPA3_HUMAN

ID UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;

DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 4.6, its MW is: 46 kDa.

DR SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENF 7
|| : ||
Db 4 FPXTDF 9

RESULT 14
TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.

RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -I- FUNCTION: Tachykinins are active peptides which excite neurons,
evoke behavioral responses, are potent vasodilators and
secreteagogues, and contract (directly or indirectly) many smooth
muscles.

CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Skin.
CC -I- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B60409; B60409.

DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroliidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
|| : ||
Db 4 PDE 6

RESULT 15

TKN1_UPERU
ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;

DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.

RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Endean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -I- FUNCTION: Tachykinins are active peptides which excite neurons,
evoke behavioral responses, are potent vasodilators and
secreteagogues, and contract (directly or indirectly) many smooth
muscles.

CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Skin.
CC -I- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroliidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 36.0%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6
|| : ||
Db 2 PDPN 5

RESULT 16

TKN2_PSEGU
ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;

DT 01-NOV-1995 (Rel. 32, Created)

```
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: Belongs to the tachykinin family.
DR PIR; C60409; C60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match
Best Local Similarity 36.0%; Score 18; DB 1; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
DB 4 PDE 6

RESULT 17
TKNS_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SP-II).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
RN [1]
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CC -|- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match
Best Local Similarity 36.0%; Score 18; DB 1; Length 11;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
DB 4 PNEFFGL 10

RESULT 18
MARI_ALTSP STANDARD; PRT; 14 AA.
ID MARI_ALTSP
AC P29399;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinstatin C-2 [Marinostatin C-1; Marinostatin D].
OS Alteromonas sp. (strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamei K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31.";
RL J. Biochem. 110:856-858(1991).
CC -|- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14 MARINOSTATIN C-2.
FT PEPTIDE 3 14 MARINOSTATIN C-1.
FT PEPTIDE 4 14 MARINOSTATIN D.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 6 7 REACTIVE BOND.
SQ SEQUENCE 14 AA; 1644 MW; 6E7CEE92E32E44 CRC64;

Query Match
Best Local Similarity 36.0%; Score 18; DB 1; Length 14;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDEN 6
DB 7 RYPSDD 12

RESULT 19
FARI_PANRE STANDARD; PRT; 8 AA.
ID FARI_PANRE
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FWRamide-like neuropeptide PFI (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=62233;
RN [1]
```

RP SEQUENCE.
 RX MEDLINE=93027659; PubMed=1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRamide-like peptides from the free-living nematode
 Panagrellus redivivus.";
 RL Peptides 13:209-214(1992).
 CC -1- FUNCTION: Myoactive.
 CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located
 CC caudally to the base of the pharynx.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 CC Neuropeptide; Amidation.
 KW MOD RES 8
 FT SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;
 SQ

Query Match 34.0%; Score 17; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENT 7
 Db 2 DPNF 5

RESULT 20
 FAR2_PANRE STANDARD; PRT; 9 AA.
 ID FAR2_PANRE
 AC P41873;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide PF2 (SADPNFURF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93027659; PubMed=1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRamide-like peptides from the free-living nematode
 Panagrellus redivivus.";
 RL Peptides 13:209-214(1992).
 CC -1- FUNCTION: Myoactive.
 CC -1- TISSUE SPECIFICITY: Nerve cords and paired groups of cells located
 CC caudally to the base of the pharynx.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 CC Neuropeptide; Amidation.
 KW MOD RES 9
 FT SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;
 SQ

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENT 7
 Db 3 DPNF 6

RESULT 21
 FAR4_CALVO STANDARD; PRT; 9 AA.
 ID FAR4_CALVO
 AC P41859;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 4.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=9219611; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 CC PIR: D41978; D41978.
 KW Neuropeptide; Amidation.
 KW MOD RES 9
 FT SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;
 SQ

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENT 7
 Db 2 PNQDF 6

RESULT 22
 URA7_HUMAN STANDARD; PRT; 10 AA.
 ID URA7_HUMAN
 AC P34950;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Erythrocyte;
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
 RA Balant L., Hochstrasser D.F.;
 RL Submitted (FEB-1994) to Swiss-Prot.
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.77, its MW is: 26 kDa.
 CC SWISS-2DPAGE; P34990; HUMAN.
 DR NON TER 10
 FT SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;
 SQ

Query Match 34.0%; Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENF 7
 Db 5 ENF 7

RESULT 23
 UXA6_CHLTR STANDARD; PRT; 10 AA.
 ID UXA6_CHLTR
 AC P38007;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christianen G., Birkelund S., Viretton E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to Swiss-Prot.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
 DR Sienna-2DPAGE; P38007; --
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NFK 8
 DB 2 NFK 4

RESULT 24
 COXA_CANFA STANDARD; PRT; 11 AA.
 ID COXA_CANFA
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COXA5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 DR HSC-2DPAGE; P99501; DOG.
 DR InterPro: IPR003204; Cyt_c_ox5A.
 DR Pfam: PF02284; COXA5A; 1.
 KM Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7
 DB 8 DEEF 11

RESULT 25
 UC04_MAIZE STANDARD; PRT; 14 AA.
 ID UC04_MAIZE
 AC P80610;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 128)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pi of this unknown
 CC protein is: 6.8, its MW is: 34.6 kDa.
 DR Maize-2DPAGE; P80610; COLEOPTILE.
 DR MaizedB; 123926; --
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1393 MW; C14451BA1116D4AD CRC64;

Query Match 34.0%; Score 17; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7
 DB 2 DEGF 5

RESULT 26
 FARI_CALVO STANDARD; PRT; 9 AA.
 ID FARI_CALVO
 AC P41856;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CallifMRamide 1.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Renfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- FUNCTION: Able to induce fluid secretion from the isolated
 CC salivary gland of Calliphora.
 CC -1- SIMILARITY: Belongs to the FARI (FMRamide related peptide)
 CC family.
 DR PIR; A41978; A41978.
 DR Neuropeptide; Amidation.
 KM MOD_RES 9
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
 DB 2 PQQDF 6

RESULT 27
FAR2_CALVO STANDARD; PRT; 9 AA.
ID FAR2_CALVO
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.,
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;
Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 PDENF 7
Db 2 PSQDF 6
RESULT 28
FAR3_CALVO STANDARD; PRT; 9 AA.
ID FAR3_CALVO
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.,
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; C41978; C41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 PDENF 7
Db 2 PSQDF 6
RESULT 29
FRF1_SARBU STANDARD; PRT; 9 AA.
ID FRF1_SARBU
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.,
RT "Identification in Drosophila melanogaster of the invertebrate G
protein-coupled FMRamide receptor.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 9
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;
Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 PDENF 7
Db 2 PSQDF 6
RESULT 30
PORB_METTM STANDARD; PRT; 10 AA.
ID PORB_METTM
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
(Fragment).
DE PORB.
GN PORB.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.,
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
in Methanobacterium thermoautotrophicum.";
RT Eur. J. Biochem. 244:862-868(1997).

CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-CoA + CO(2) + reduced ferredoxin.
 CC -1- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one gamma chain.
 CC -1- MISCELLANEOUS: Has a pH optimum of 10.0 and an optimal temperature of 80 degrees Celsius.
 KM Oxidoreductase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
 Db 4 PEQXF 8

RESULT 31
 PPCK_FASHE STANDARD; PRT; 10 AA.
 ID PPCK_FASHE STANDARD; PRT; 10 AA.
 AC P80525;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)
 DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile protein 1) (Fragment).
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Fasciolidae; Fasciola.
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9536693; PubMed=7639732;
 RA Tkalcic J., Ashman K., Meusen E.;
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile proteins."
 RT Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate + CO(2).
 CC -1- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase [GTP] family.
 CC InterPro: IPR008209; PEP_carboxykin.
 DR PROSITE: PS00505; PEPCK_GTP; PARTIAL.
 KM Lyase; Decarboxylase; GTP-binding.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.3e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
 Db 1 YPD 3

RESULT 32
 MP1_MICOC STANDARD; PRT; 13 AA.
 ID MP1_MICOC STANDARD; PRT; 13 AA.
 AC P81532;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE MP1 protein (Fragments).
 OS Microplitis ocellatae (Braconid wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae; Braconidae; Microgasterinae; Microplitis.
 OX NCBI_TaxID=99573;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Larva;
 RA Takahashi M., Quicke D.L.J.;
 RL Submitted (OCT-1998) to Swiss-Prot.
 CC -1- TISSUE SPECIFICITY: Salivary glands.
 CC -1- DEVELOPMENTAL STAGE: LARVAL.
 FT NON CONS 10 11
 SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 32.0%; Score 16; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 3e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENF 7
 Db 6 YPVPVY 11

RESULT 33
 ATP6_SPIOL STANDARD; PRT; 14 AA.
 ID ATP6_SPIOL STANDARD; PRT; 14 AA.
 AC P80086;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP synthase A chain (EC 3.6.3.14) (Protein 6) (Fragment).
 GN ATP6.
 OS Spinacia oleracea (Spinach).
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=cv. Medania; TISSUE=leaf mesophyll;
 RX MEDLINE=92209531; PubMed=1313368;
 RA Hamasur B., Glaser E.;
 RT "Plant mitochondrial F0F1 ATP synthase. Identification of the individual subunits and properties of the purified spinach leaf mitochondrial ATP synthase."
 RT Eur. J. Biochem. 205:409-416(1992).
 CC -1- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the ATPase A chain family.
 DR InterPro: IPR000568; ATPsynt_Asub.
 DR PROSITE: PS00449; ATPASE_A; PARTIAL.
 KM Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1619 MW; 9F1D60181FC1FF45 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 14;
 Best Local Similarity 42.9%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENFKL 9
 Db 2 PLEQFSI 8

RESULT 34
 ALL6_CYDPO STANDARD; PRT; 8 AA.
 ID ALL6_CYDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PDENF 9
DB 2 PLYNFG 8

RESULT 35
FARS_CALVO
ID FARS CALVO STANDARD; PRT; 9 AA.
AC P41860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 5.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; E41978; E41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1068 MW; 39D10699CAB6D867 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 PDENF 7
DB 2 PGQDF 6

RESULT 36
FARA_CALVO
ID FARA CALVO STANDARD; PRT; 9 AA.
AC P41865;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 10.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; A44787; A44787.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ UNSTRE 1 1 OR S OR A.
FT SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 PDENF 7
DB 2 PNRDF 6

RESULT 37
Q2OB_COMTE
ID Q2OB COMTE STANDARD; PRT; 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxidoeductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Felzner S., Lingens F.;
RT "Quinolone 2-oxidoeductase and 2-oxo-1,2-dihydroquinoline 5,6-
dioxygenase from Comamonas testosteroni 63. The first two enzymes in
quinolone and 3-methylquinoline degradation."
RL Eur. J. Biochem. 232:536-544(1995).
CC -1- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)-2-oxo-1,2-
dihydroquinoline.
CC -1- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isouinolone-
1(2H)-one + reduced acceptor.
CC -1- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -1- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
step.
CC -1- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
two gamma chains (Probable).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON TER 10
FT SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3
: ||
Db 2 KFP 4

RESULT 38

UPA2_HUMAN
ID UPA2_HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.4, its MW is: 49 kDa.
DR SWISS-2DPAGE; P30088; HUMAN.
FT NON TER 1 1
FT UNSTRE 6 6
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB7775B7 CRC64;
Query Match 30.0%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
: ||
Db 6 PDD 8

RESULT 39

TKNA_RANCA
ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine."
RL Regul. Pept. 46:81-88(1993).
CC -I- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the tachykinin family.
DR PIR, A61033; A61033.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;
Query Match 30.0%; Score 15; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.9e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PDENFKL 9
: ||
Db 4 PDREYGL 10

RESULT 40

FARI_CALVO
ID FARI_CALVO STANDARD; PRT; 12 AA.
AC P41869;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Callimorfamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -I- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR PIR, E44787; E44787.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6
: ||
Db 5 PSDN 8

RESULT 41

TKN1_KASMA
ID TKN1_KASMA STANDARD; PRT; 12 AA.
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hylambates kassinin ([Glu2,Pro5]kassinin).
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hyalambates-kassinin) and
hyalambatin, in the skin of the African rhacophorid frog Hyalambates
maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S10059; S10059.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KM Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12
SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
Db 5 PDQ 7

RESULT 42
ADFB_TENMO STANDARD; PRT; 13 AA.
ID ADFB_TENMO
AC P83109;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor B (ADFB).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=22465067; PubMed=12576082;
RA Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
RA Hull J.J., Schooley D.A.;
RT "Isolation, identification and localization of a second beetle
RT antidiuretic peptide.";
RL Peptides 24:27-34(2003).
CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
CC cGMP as second messenger. May function as an antidiuretic
CC hormone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
CC pairs of bilaterally symmetrical cells in the protocerebrum.
CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
KM Neuropeptide; Hormone.
SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;

Query Match 30.0%; Score 15; DB 1; Length 13;
Best Local Similarity 28.6%; Pred. No. 4.7e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8
Db 1 YDDGSYX 7

RESULT 43
LPAA_PORGI STANDARD; PRT; 13 AA.
ID LPAA_PORGI
AC P81411;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Lipid-A-associated protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=W50;
RX MEDLINE=99061194; PubMed=9846737;
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
RA Curtis M., Henderson B., Tabona P.;
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived
RT from the haemagglutinating domain of the RI protease gene family, is
RT a potent stimulator of interleukin 6 synthesis.";
RL Microbiology 144:3019-3026(1998).
CC -1- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
CC THAT ANCHORS THE LIPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
CC CELL.
CC VARIANT 12 12 G -> F.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6
Db 6 PDKD 9

RESULT 44
LCK3_LEUMA STANDARD; PRT; 8 AA.
ID LCK3_LEUMA
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.U.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctodeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 510 MW; DC6365B449C866DA CRC64;

Query Match 28.0%; Score 14; DB 1; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7
| : |
Db 1 DOGF 4

RESULT 45

SAMP_MUSCA

ID SAMP MUSCA STANDARD; PRT; 9 AA.

AC P19055;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum amyloid P-component (SAP) (Fragment).

OS Mustelus canis (Smooth dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;

OC Mustelus.

OX NCBI_TaxID=7812;

RN [1]

RP SEQUENCE.

RX MEDLINE=83160332; Pubmed=6403520;

RA Robey F.A., Tanaka T., Liu T.-Y.;

RT "Isolation and characterization of two major serum proteins from the

RT dogfish, Mustelus canis, C-reactive protein and amyloid P

RT component.";

RL J. Biol. Chem. 258:3889-3894(1983).

CC -1- SUBUNIT: Homopentamer. Pentaxin (or pentraxin) have a discoid

CC arrangement of 5 noncovalently bound subunits.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND

CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.

CC -1- SIMILARITY: Belongs to the pentaxin family.

DR InterPro; IPR001759; Pentaxin.

DR PROSITE; PS00289; PENTAXIN; PARTIAL.

KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.

FT DOMAIN 1 >9 PENTAXIN.

FT NON TER 9 9

SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match

Best Local Similarity 28.0%; Score 14; DB 1; Length 9;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPDEN 6
| : |
Db 2 PPGKS 6

Search completed: August 30, 2004, 10:50:23
Job time : 2.55068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-7
Perfect score: 50
Sequence: 1 RFPDENPKL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	46.0	11	2	E60409 substance P-like p
2	20	40.0	13	2	S29488 GTP-binding protei
3	20	40.0	14	2	A42473 ermK leader peptid
4	20	40.0	14	2	S58862 botulinum neurotox
5	20	40.0	14	2	S58866 botulinum neurotox
6	20	40.0	14	2	PH1757 T cell receptor al
7	20	40.0	14	2	PH1758 T cell receptor al
8	20	40.0	14	2	PH1759 T cell receptor al
9	20	40.0	14	2	PH1766 T cell receptor al
10	20	40.0	14	2	PH1767 T cell receptor al
11	20	40.0	14	2	PH1768 T cell receptor al
12	20	40.0	14	2	PH1769 T cell receptor al
13	19	38.0	10	2	A60476 S-layer protein -
14	18	36.0	8	2	PH1407 Ig heavy chain V r
15	18	36.0	8	2	A39892 element, P cytot
16	18	36.0	9	2	S10784 enamel in 1 - bovin
17	18	36.0	10	2	B33710 ornithine decarbox
18	18	36.0	10	2	PQ0753 beta-fructofuranos
19	18	36.0	11	2	F60409 substance P-like p
20	18	36.0	11	2	B60409 kassinin-like pept
21	18	36.0	11	2	C60409 kassinin-like pept
22	18	36.0	11	2	S07203 uperolein - frog
23	18	36.0	14	2	A54370 inorganic diphosph
24	17	34.0	9	2	G58502 kidney and bladder
25	17	34.0	10	2	D41978 califMRamide 4 -
26	17	34.0	10	2	A61354 carnitine medium/1
27	17	34.0	11	2	UQ2307 hypothetical 1.5K
28	17	34.0	12	2	A61309 glycoprotein hormo
29	17	34.0	12	2	A56878 light yellow cell

30	17	34.0	12	2	PH1462 T-cell receptor be
31	17	34.0	14	2	A41589 25K elastin-bindin
32	16	32.0	9	2	A41978 califFMRamide 1 -
33	16	32.0	9	2	B41978 califFMRamide 2 -
34	16	32.0	9	2	C41978 califFMRamide 3 -
35	16	32.0	9	2	B49712 ATP-binding protei
36	16	32.0	10	2	S19296 16K protein - poul
37	16	32.0	12	2	S15815 translation elonga
38	16	32.0	13	2	S47373 T-cell antigen rec
39	16	32.0	14	2	S21247 H+-transporting tw
40	16	32.0	14	2	S29632 avenin alpha-2 - o
41	16	32.0	14	2	S29632 xylan 1,4-beta-xy
42	16	32.0	14	2	P50371 hypothetical prote
43	15	30.0	8	2	A46306 spasmodic toxin
44	15	30.0	8	2	A14683 aspartate transam
45	15	30.0	8	2	S29272 tocopherol-binding

ALIGNMENTS

RESULT 1
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C/Species: Pseudophryne guentheri
C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C/Accession: E60409
R/Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austral
A/Reference number: A60409; MUID:90287814; PMID:2356157
A/Accession: E60409
A/Molecule type: protein
A/Residues: 1-11 <SIM>
C/Superfamily: unassigned animal peptides
C/Keywords: amidated carboxyl end; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 46.0%; Score 23; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENPKL 9
DB 4 PDEFFGL 10

RESULT 2
S29488
GTP-binding protein o-rab3 - marbled electric ray (fragment)
C/Species: Torpedo marmorata (marbled electric ray)
C/Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C/Accession: S29488
R/Volkhardt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A/Reference number: S29485; MUID:93154521; PMID:8428634
A/Accession: S29488
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <VOL>

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 13;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENF 7
DB 5 DONF 8

RESULT 3

A42473
ermK leader peptide - Bacillus licheniformis
C/Species: Bacillus licheniformis
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Sep-1999
C/Accession: A42473; 139884
R/Kwak, J.H.; Choi, E.C.; Weisblum, B.
J. Bacteriol. 173, 4725-4735, 1991
A/Title: Transcriptional attenuation control of ermK, a macrolide-lincosamide-streptogramin B resistance determinant
A/Reference number: A42473; MUID:91310580; PMID:1713206
A/Accession: A42473
A/Molecule type: DNA
A/Residues: 1-14 <KMA>
R/Gryczan, T.; Israeli-Reches, M.; Del Bue, M.; Dubnau, D.A.
Mol. Gen. Genet. 194, 349-356, 1984
A/Title: DNA sequence and regulation of ermD, a macrolide-lincosamide-streptogramin B resistance determinant
A/Reference number: 139884; MUID:84245158; PMID:6429477
A/Accession: 139884
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-14 <RES>
A/Cross-references: GB:M29832; NID:g143199; PIDN:AAA22598.1; PID:g143200
C/Superfamily: unassigned leader peptides

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RFPDEN 6
DB 8 RFPDEN 13

RESULT 4
S58862
botulinum neurotoxin type A and B hemagglutinin component II - Clostridium botulinum (strain NCTC 7273)
N/Alternate names: HA-II protein
C/Species: Clostridium botulinum
C/Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 15-Oct-1999
C/Accession: S58862; S58858
R/East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A/Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin
A/Reference number: S58855
A/Accession: S58862
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-14 <EAS>
A/Cross-references: EMBL:X79104; NID:g870937; PIDN:CAAS5719.1; PID:g870941
A/Experimental source: strain NCTC 7272
A/Accession: S58858
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-14 <EA2>
A/Cross-references: EMBL:X79103; NID:g870932; PIDN:CAAS5715.1; PID:g870936
A/Experimental source: strain Eklund 17B
C/Keywords: hemagglutinin; neurotoxin

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
DB 9 PNGNYK 14

RESULT 5
S58866
botulinum neurotoxin type B hemagglutinin component II - Clostridium botulinum (NCTC 7273)
N/Alternate names: protein HA-II
C/Species: Clostridium botulinum
A/Variety: NCTC 7273
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999

C/Accession: S58866
R/East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A/Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin
A/Reference number: S58855
A/Accession: S58866
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-14 <EAS>
A/Cross-references: EMBL:X79102; NID:g870942; PIDN:CAAS5711.1; PID:g870946
A/Experimental source: NCTC 7273
C/Keywords: hemagglutinin; neurotoxin

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
DB 9 PNGNYK 14

RESULT 6
PH1757
T cell receptor alpha chain V region (clone 1V alpha 7.2-1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1757
R/Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood mononuclear cells
A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1757
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <POR>

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
DB 6 DSNYQL 11

RESULT 7
PH1758
T cell receptor alpha chain V region (clone 1V alpha 7.2-2) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1758
R/Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood mononuclear cells
A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1758
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <POR>

Query Match
Best Local Similarity 40.0%; Score 20; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
DB 6 DSNYQL 11

RESULT 8

PH1759
T cell receptor alpha chain V region (clone 1V alpha 7.2-3) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1759

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1759

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <POR>

Query Match 40.0%; Score 20; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENFKL 9

Db 6 DSNYQL 11

RESULT 9

PH1766
T cell receptor alpha chain V region (clone 2V alpha 7.2-1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1766

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1766

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <POR>

Query Match 40.0%; Score 20; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENFKL 9

Db 6 DSNYQL 11

RESULT 10

PH1767
T cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1767

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1767

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <POR>

Query Match 40.0%; Score 20; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENFKL 9

Db 6 DSNYQL 11

RESULT 11

PH1768
T cell receptor alpha chain V region (clone 2V alpha 7.2-3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1768

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1768

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <POR>

Query Match 40.0%; Score 20; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENFKL 9

Db 6 DSNYQL 11

RESULT 12

PH1769
T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1769

R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1769

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <POR>

Query Match 40.0%; Score 20; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 DENFKL 9

Db 6 DSNYQL 11

RESULT 13

A60476
S-layer protein - Bacillus thuringiensis (fragment)

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993

C:Accession: A60476

R:Luckevich, M.D.; Beveridge, T.J.

J. Bacteriol. 171, 6656-6667, 1989

A:Title: Characterization of a dynamic S layer on Bacillus thuringiensis.

A:Reference number: A60476; MUID:90078111; PMID:2592346

A:Accession: A60476

A:Molecule type: protein

A:Residues: 1-10 <LUC>

C:Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 38.0%; Score 19; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FPD 4

Db 5 FPD 7

RESULT 14

PH1407
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C/Accession: PH1407
R/Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Teraoka, Y. Exp. Med. 176, 1209-1214, 1992
A/Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in a virus.
A/Reference number: PH1403; MUID:93018837; PMID:1402663
A/Accession: PH1407
A/Molecule type: DNA
A/Residues: 1-8 <SH1>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 36.0%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3
Db 6 RFP 8

RESULT 15

A39892
P element, P cytotype-determining - fruit fly (Drosophila melanogaster) (fragment)
C/Species: Drosophila melanogaster
C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997
C/Accession: A39892
R/Nitazaka, E.; Mukai, T.; Yamazaki, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987
A/Title: Repressor of P elements in Drosophila melanogaster: cytotype determination by a
A/Reference number: A39892
A/Accession: A39892
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-8 <NIT>
C/Genetics:
A/Gene: FlyBase:P-element
A/Cross-references: FlyBase:FBgn0003055

Query Match 36.0%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENFK 8
Db 3 KNFK 6

RESULT 16

S10784
enamelin i - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C/Accession: S10784
R/Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A/Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A/Reference number: S10780; MUID:90336641; PMID:2379503
A/Accession: S10784
A/Molecule type: protein
A/Residues: 1-9 <STR>
C/Keywords: enamel; phosphoprotein

Query Match 36.0%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENF 7
Db 1 FPDGF 6

RESULT 17

B33710
ornithine decarboxylase leader peptide - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 24-Sep-1999
C/Accession: B33710
R/Wen, L.; Huang, J.K.; Blackshear, P.J.
J. Biol. Chem. 264, 9016-9021, 1989
A/Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory elem
A/Reference number: A33710; MUID:89255378; PMID:2722815
A/Accession: B33710
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A/Molecule type: mRNA
A/Residues: 1-10 <WEN>
A/Cross-references: GB:J04791; NID:G205807; PIDN:AAA66163.1; PID:G806309
C/Superfamily: unassigned leader peptides

Query Match 36.0%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFP 3
Db 6 RFP 8

RESULT 18

PQ0753
beta-fructofuranosidase (EC 3.2.1.26) IIB - barley (fragment)
C/Species: Hordeum vulgare (barley)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 23-Mar-1995
C/Accession: PQ0753
R/Oberland, D.M.; Simmen, U.; Boller, T.; Wiemken, A.
Plant Physiol. 101, 1331-1339, 1993
A/Title: Purification and characterization of three soluble invertases from barley (Horde
A/Reference number: PQ0752; MUID:94143483; PMID:8310063
A/Accession: PQ0753
A/Molecule type: protein
A/Residues: 1-10 <OBE>
A/Experimental source: leaf, cv. Express
C/Keywords: alternative initiators; glycoprotein; glycosidase; hydrolase

Query Match 36.0%; Score 18; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
Db 2 FPDNTML 9

RESULT 19

F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C/Species: Pseudophryne guentheri
C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C/Accession: F60409
R/Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri
Peptides 11, 299-304, 1990
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia
A/Reference number: A60409; MUID:90287814; PMID:2356157
A/Accession: F60409
A/Molecule type: protein
A/Residues: 1-11 <SIM>
C/Superfamily: unassigned animal peptides
C/Keywords: amidated carboxyl end; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
|||
Db 4 PNEPFGI 10

RESULT 20

B60409
kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C:Accession: B60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: B60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>

A>Note: this peptide was also found in a deamidated form
C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
|||
Db 4 PDE 6

RESULT 21

C60409

kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C:Accession: C60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: C60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>

A>Note: this peptide was also found in a deamidated form
C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
|||
Db 4 PDE 6

RESULT 22

S07203

uperolein - frog (Uperoleia marmorata)

C:Species: Uperoleia marmorata
C>Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07203

R:Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975
A>Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin of

A:Reference number: S07203; MUID:75131227; PMID:1120493

A:Accession: S07203

A:Molecule type: protein
A:Residues: 1-11 <ANA>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDEN 6
|||
Db 2 PDPN 5

RESULT 23

A54370

Inorganic diphosphatase (EC 3.6.1.1) - cucurbit (fragment)

C:Species: Cucurbita sp. (cucurbit)

C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 03-Jun-2002

C:Accession: A54370

R:Sato, M.H.; Kasahara, M.; Ishii, N.; Homareda, H.; Matsui, H.; Yoshida, M.

J. Biol. Chem. 269, 6725-6728, 1994

A>Title: Purified vacuolar inorganic pyrophosphatase consisting of a 75-kDa polypeptide

A:Reference number: A54370; MUID:94165068; PMID:8120031

A:Accession: A54370

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SAT>

C:Keywords: hydrolase

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDE 5
|||
Db 11 PDE 13

RESULT 24

G58502

kidney and bladder stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C:Accession: G58502

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: G58502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <BIN>

A:Experimental source: human kidney stone, bladder stone

A>Note: a secondary sequence AAKENPXD was also found

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENF 7
|||
Db 3 PDVKF 7

RESULT 25

D41978
calliFMRamide 4 - bluebottle fly (Calliphora vomitoria)
C/Species: Calliphora vomitoria
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: D41978
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A/Reference number: A41978; MUID:92196111; PMID:1549595
A/Accession: D41978
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <DUV>
C/Keywords: amidated carboxyl end; neuropeptide
F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENF 7
|::|
Db 2 PNDGF 6

RESULT 26
A61354
carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
N/Alternate names: endoplasmic reticulum protein ERP61; glucose regulated protein GRP58;
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C/Accession: A61354
R/Murthy, M.S.R.; Pande, S.V.
Mol. Cell. Biochem. 122, 133-138, 1993
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previ
A/Reference number: A61354; MUID:94049728; PMID:8232244
A/Accession: A61354
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <MUR>
C/Keywords: acyltransferase

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DEN 6
|||
Db 8 DEN 10

RESULT 27
JQ2307
hypothetical 1.5K protein - tomato chloroplast (strain Toko)
C/Species: chloroplast Lycopersicon esculentum (tomato)
C/Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 23-Mar-1995
C/Accession: JQ2307
R/Kawagoe, Y.; Kikuta, Y.
Theor. Appl. Genet. 81, 13-20, 1991
A/Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
A/Reference number: JQ2306
A/Accession: JQ2307
A/Molecule type: DNA
A/Residues: 1-11 <KAW>
A/Experimental source: strain Toko
C/Genetics:
A/Genome: chloroplast
C/Keywords: chloroplast

Query Match 34.0%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENF 7
|||
Db 5 DEBF 8

RESULT 28
A61309
glycoprotein hormones alpha chain - hamster (fragment)
N/Alternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; lutr
C/Species: Cricetinae gen. sp. (hamster)
C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C/Accession: A61309
R/Gleim, S.D.; Nahn, H.S.; Greenwald, G.S.; Ward, D.N.
Endocrinology 111, 1263-1269, 1982
A/Title: Isolation and characterization of hamster luteinizing hormone.
A/Reference number: A61309; MUID:83003498; PMID:6889489
A/Accession: A61309
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <GLE>
C/Superfamily: glycoprotein hormones alpha chain
C/Keywords: glycoprotein

Query Match 34.0%; Score 17; DB 2; Length 12;
Best Local Similarity 28.6%; Pred. No. 3.6e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
|::|
Db 2 PBGDFTM 8

RESULT 29
A56878
light yellow cell peptide A - great pond snail
N/Contains: light yellow cell peptide B
C/Species: Lymnaea stagnalis (great pond snail)
C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Aug-1999
C/Accession: A56878
R/Hoek, R.M.; Li, K.W.; van Minnen, J.; Geraerts, W.P.
Brain Res. Mol. Brain Res. 16, 71-74, 1992
A/Title: Chemical characterization of a novel peptide from the neuroendocrine light yell
A/Reference number: A56878; MUID:93095719; PMID:1334202
A/Accession: A56878
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <HOE>
A/Cross-references: PIDN:AB24433.1; PID:g261422
A/Note: sequence extracted from NCBI backbone (NCBIP:120090)
C/Keywords: neuropeptide
F/1-12/Product: light yellow cell peptide A #status experimental <YCPA>
F/2-12/Product: light yellow cell peptide B #status experimental <YCPB>

Query Match 34.0%; Score 17; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 3.6e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENFKL 9
||:|
Db 3 PDKSILL 9

RESULT 30
PH1462
T-cell receptor beta chain (clone A24/PEF1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C/Accession: PH1462
R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A/Title: T cell receptor selection by and recognition of two class I major histocompatib
A/Reference number: PH1430; MUID:93171821; PMID:8436911
A/Accession: PH1462

A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Experimental source: cytolytic T-lymphocyte
C/Superfamily: immunoglobulin homology
C/Keywords: receptor; T-cell

Query Match 34.0%; Score 17; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PDENF 7
|:|
Db 7 PDYTF 11

RESULT 31

A41589
25K elastin-binding protein - Staphylococcus aureus (fragment)
C/Species: Staphylococcus aureus
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Mar-1993
C/Accession: A41589
R/Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.; Me
J. Biol. Chem. 266, 23399-23406, 1991
A/Title: Binding of elastin to Staphylococcus aureus.
A/Reference number: A41589; MUID:92078218; PMID:1744133
A/Accession: A41589
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <PAR>

Query Match 34.0%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NFK 8
|||
Db 3 NFK 5

RESULT 32

A41978
CalliFMRamide 1 - bluebottle fly (Calliphora vomitoria)
C/Species: Calliphora vomitoria
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: A41978
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A/Reference number: A41978; MUID:92196111; PMID:1549595
A/Accession: A41978
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <DUV>
C/Keywords: amidated carboxyl end; neuropeptide
F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
|:|
Db 2 PQQDF 6

RESULT 33

B41978
calliFMRamide 2 - bluebottle fly (Calliphora vomitoria)
C/Species: Calliphora vomitoria
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: B41978
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A/Reference number: A41978; MUID:92196111; PMID:1549595

A/Accession: B41978
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <DUV>
C/Keywords: amidated carboxyl end; neuropeptide
F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
|:|
Db 2 PQQDF 6

RESULT 34

C41978
calliFMRamide 3 - bluebottle fly (Calliphora vomitoria)
C/Species: Calliphora vomitoria
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: C41978
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe,
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A/Reference number: A41978; MUID:92196111; PMID:1549595
A/Accession: C41978
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <DUV>
C/Keywords: amidated carboxyl end; neuropeptide
F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENF 7
|:|
Db 2 PQQDF 6

RESULT 35

B49712
ATP-binding protein p46 - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C/Accession: B49712
R/Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
J. Biol. Chem. 269, 1744-1749, 1994
A/Title: A set of endoplasmic reticulum proteins possessing properties of molecular chap
A/Reference number: A49712; MUID:94124514; PMID:8294423
A/Accession: B49712
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <NIG>
C/Keywords: ATP; endoplasmic reticulum; molecular chaperone

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPD 4
|:|
Db 5 YPD 7

RESULT 36

S19296
16k protein - poulard wheat
C/Species: Triticum turgidum (poulard wheat)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C/Accession: S19296
R/Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.
Biochem. J. 281, 401-405, 1992
A/Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subunit
A/Reference number: S19296; MUID:92143804; PMID:1736890
A/Accession: S19296
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <SAN>

Query Match
Best Local Similarity 32.0%; Score 16; DB 2; Length 10;
Matches 2; Conservativity 50.0%; Pred. No. 4.7e+03;
Matches 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PDEN 6
Db 3 PDQS 6

RESULT 37

S15815
translation elongation factor eEF-2 - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 18-Mar-1997
C/Accession: S15815; S12970
R/Price, N.T.; Redpath, N.T.; Severinov, K.V.; Campbell, D.G.; Russell, J.M.; Proud, C.G.
FEBS Lett. 282, 253-258, 1991
A/Title: Identification of the phosphorylation sites in elongation factor-2 from rabbit
A/Reference number: S15815; MUID:91243806; PMID:2037042
A/Accession: S15815
A/Molecule type: protein
A/Residues: 1-12 <UMP>
R/Ovchinnikov, L.P.; Motuz, L.P.; Natapov, P.G.; Averbuch, L.J.; Wettenthal, R.E.H.; Szy
FEBS Lett. 275, 209-212, 1990
A/Title: Three phosphorylation sites in elongation factor 2.
A/Reference number: S12970; MUID:91085562; PMID:2261989
A/Accession: S12970
A/Molecule type: protein
A/Residues: 2-12 <OVC>
C/Superfamily: translation elongation factor 2; translation elongation factor Tu homolog
C/Keywords: GTP binding; phosphoprotein; protein biosynthesis
F/8,10/Binding site: phosphate (Thr) (covalent) (by elongation factor 2 kinase) #status

Query Match
Best Local Similarity 32.0%; Score 16; DB 2; Length 12;
Matches 3; Conservativity 75.0%; Pred. No. 5.7e+03;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RFPD 4
Db 6 RFTD 9

RESULT 38

S47373
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47373
R/Lehner, P.U.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
A/Reference number: S47355
A/Accession: S47373
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35672; NID:G527489; PIDN:CAA84741.1; PID:G527490
C/Keywords: T-cell receptor

Query Match
Best Local Similarity 32.0%; Score 16; DB 2; Length 13;
Matches 3; Conservativity 42.9%; Pred. No. 6.2e+03;
Matches 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RFPDENF 7
Db 6 RSDADEXY 12

RESULT 39

S21247
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - spinach mitochondrion (fragme
N/Alternate names: 18.5K protein
C/Species: mitochondrion Spinacia oleracea (spinach)
C/Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 03-Jun-2002
C/Accession: S21247
R/Hamasur, B.; Glaser, E.
Eur. J. Biochem. 205, 409-416, 1992
A/Title: Plant mitochondrial F(0)F(1) ATP synthase. Identification of the individual sub
A/Reference number: S21204; MUID:92209531; PMID:1313368
A/Accession: S21247
A/Molecule type: protein
A/Residues: 1-14 <HAM>
A/Experimental source: leaf
C/Genetics:
A/Genome: mitochondrion
C/Superfamily: H+-transporting ATP synthase protein 6
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi

Query Match
Best Local Similarity 32.0%; Score 16; DB 2; Length 14;
Matches 3; Conservativity 42.9%; Pred. No. 6.7e+03;
Matches 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 PDENFKL 9
Db 2 PLEQFSI 8

RESULT 40

S29209
avenin alpha-2 - oat (fragment)
N/Alternate names: CIP-3; coeliac immunoreactive protein 3
C/Species: Avena sativa (oat)
C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C/Accession: S29209
R/Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A/Title: Identification of the three major coeliac immunoreactive proteins and one alpha-
A/Reference number: S29207; MUID:92405739; PMID:1526282
A/Accession: S29209
A/Molecule type: protein
A/Residues: 1-14 <ROC>
A/Experimental source: endosperm
C/Superfamily: gliadin
C/Keywords: prolamin; seed

Query Match
Best Local Similarity 32.0%; Score 16; DB 2; Length 14;
Matches 2; Conservativity 33.3%; Pred. No. 6.7e+03;
Matches 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 PDENFK 8
Db 8 PSEQYQ 13

RESULT 41

S29632
xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Thermotoga sp. (strain FjSS3-B.1) (fragment)
N/Alternate names: beta-xylosidase
C/Species: Thermotoga sp.
A/Variety: FjSS3-B.1
C/Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999
C/Accession: S29632
R/Ruttersmith, L.D.; Daniel, R.M.
Biochim. Biophys. Acta 1156, 167-172, 1993
A/Title: Thermostable beta-glucosidase and beta-xylosidase from Thermotoga sp. strain Fj

A;Reference number: S29631; MUID:93152594; PMID:8427876

A;Accession: S29632

A;Molecule type: protein

A;Residues: 1-14 <RUT>

A;Experimental source: strain FJSS3-B.1

C;Comment: Although the beta-xylosidase enzyme activity was apparently confirmed for this

C;Function:

A;Description: hydrolyzes short chain oligosaccharides and xylobiose to produce D-xylose

A;Note: plays an important role in the relief of end-product inhibition of endoxylanase

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match

32.0%; Score 16; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDE 5

DB 8 FADE 11

RESULT 42

PS0371

hypothetical protein (psac region) - *Synechococcus* sp. (fragment)

C;Species: *Synechococcus* sp.

C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999

C;Accession: PS0371

R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.

Gene 112, 123-128, 1992

A;Title: The psac genes of *Synechococcus* sp. PCC7002 and *Cyanophora paradoxa*: cloning an

A;Reference number: JS0694; MUID:92201692; PMID:1551590

A;Accession: PS0371

A;Molecule type: DNA

A;Residues: 1-14 <RHI>

A;Cross-references: GB:M66238; NID:9154574; PIDN:AAA27351.1; PID:9552030

Query Match

32.0%; Score 16; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ENFKL 9

DB 2 KGFKL 6

RESULT 43

A46306

spasmogenic toxin PNVI - spider (*Phoneutria nigriventer*) (fragment)

C;Species: *Phoneutria nigriventer*

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999

C;Accession: A46306

R;Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.

Toxicon 31, 377-384, 1993

A;Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide

A;Reference number: A46306; MUID:93276438; PMID:8503129

A;Accession: A46306

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <MAR>

Query Match

30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPDEN 6

DB 3 FPGQS 7

RESULT 44

A14683

aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm

N;Alternate names: aspartate aminotransferase, mitochondrial

C;Species: *Gallus gallus* (chicken)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000

C;Accession: A14683

R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.

FEBS Lett. 108, 98-102, 1979

A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.

A;Reference number: A14683; MUID:80092116; PMID:520566

A;Accession: A14683

A;Molecule type: protein

A;Residues: 1-8 <WIL>

C;Keywords: aminotransferase; mitochondrion

Query Match

30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFK 8

DB 2 ENNFQ 6

RESULT 45

S29272

tocopherol-binding protein, 81K - rat (fragment)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996

C;Accession: S29272

R;Nalecz, K.A.; Nalecz, M.J.; Azzi, A.

Eur. J. Biochem. 209, 37-42, 1992

A;Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r5

A;Reference number: S29272; MUID:9301150; PMID:1396710

A;Accession: S29272

A;Molecule type: protein

A;Residues: 1-8 <NAL>

A;Experimental source: smooth muscle A7r5 cells

Query Match

30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6

DB 1 PEED 4

Search completed: August 30, 2004, 10:58:51
Job time : 2.70608 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0068 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-7
Perfect score: 50
Sequence: 1 RFPDENFKL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	30	60.0	9	16	US-10-264-309-118 Sequence 118, App
2	29	58.0	9	12	US-09-988-493-293 Sequence 293, App
3	29	58.0	9	12	US-10-014-340-209 Sequence 209, App
4	29	58.0	10	14	US-10-062-109A-328 Sequence 328, App
5	29	58.0	10	14	US-10-005-480A-328 Sequence 328, App
6	29	58.0	14	10	US-09-880-748-2437 Sequence 2437, App
7	29	58.0	14	10	US-09-880-748-2437 Sequence 2437, App
8	29	58.0	14	12	US-10-293-418-2684 Sequence 2684, App
9	29	58.0	14	12	US-10-293-418-2684 Sequence 2684, App
10	27	54.0	8	14	US-10-226-629A-464 Sequence 464, App
11	27	54.0	8	14	US-10-226-629A-477 Sequence 477, App
12	27	54.0	9	10	US-09-938-864-36 Sequence 36, App1
13	27	54.0	9	10	US-09-791-477-36 Sequence 36, App1
14	27	54.0	9	10	US-09-785-019-36 Sequence 36, App1
15	27	54.0	9	14	US-10-125-635A-36 Sequence 36, App1

16	27	54.0	9	14	US-10-002-603-36 Sequence 36, App1
17	27	54.0	9	14	US-10-062-109A-7 Sequence 7, App1
18	27	54.0	9	14	US-10-062-109A-560 Sequence 560, App
19	27	54.0	9	14	US-10-226-629A-465 Sequence 465, App
20	27	54.0	9	14	US-10-226-629A-478 Sequence 478, App
21	27	54.0	9	14	US-10-226-629A-491 Sequence 491, App
22	27	54.0	9	14	US-10-005-480A-7 Sequence 7, App1
23	27	54.0	9	14	US-10-005-480A-560 Sequence 560, App
24	27	54.0	9	14	US-10-195-835-36 Sequence 36, App1
25	27	54.0	9	15	US-10-244-830-36 Sequence 36, App1
26	27	54.0	9	15	US-10-244-830-36 Sequence 36, App1
27	27	54.0	9	15	US-10-427-717-36 Sequence 36, App1
28	27	54.0	9	16	US-10-648-780-36 Sequence 36, App1
29	27	54.0	10	14	US-10-062-109A-196 Sequence 196, App
30	27	54.0	10	14	US-10-062-109A-427 Sequence 427, App
31	27	54.0	10	14	US-10-062-109A-507 Sequence 507, App
32	27	54.0	10	14	US-10-062-109A-614 Sequence 614, App
33	27	54.0	10	14	US-10-226-629A-466 Sequence 466, App
34	27	54.0	10	14	US-10-226-629A-479 Sequence 479, App
35	27	54.0	10	14	US-10-226-629A-492 Sequence 492, App
36	27	54.0	10	14	US-10-226-629A-505 Sequence 505, App
37	27	54.0	10	14	US-10-005-480A-196 Sequence 196, App
38	27	54.0	10	14	US-10-005-480A-427 Sequence 427, App
39	27	54.0	10	14	US-10-005-480A-507 Sequence 507, App
40	27	54.0	10	14	US-10-005-480A-614 Sequence 614, App
41	27	54.0	11	14	US-10-226-629A-467 Sequence 467, App
42	27	54.0	11	14	US-10-226-629A-480 Sequence 480, App
43	27	54.0	11	14	US-10-226-629A-493 Sequence 493, App
44	27	54.0	11	14	US-10-226-629A-506 Sequence 506, App
45	27	54.0	11	14	US-10-226-629A-518 Sequence 518, App

ALIGNMENTS

RESULT 1
US-10-264-309-118
; Sequence 118, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLF, CHRISTIAN
; APPLICANT: SNIDER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-118
Query Match 60.0%; Score 30; DB 16; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
| | | | |
Db 1 FEDENFLL 8

RESULT 2

US-09-988-493-293
; Sequence 293, Application US/09988493
; Publication No. US20030064419A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseleage Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-293

Query Match 58.0%; Score 29; DB 12; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
| | | | |
Db 1 FEDENFLL 8

RESULT 3

US-10-014-340-209
; Sequence 209, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 209
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-209

Query Match 58.0%; Score 29; DB 12; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
| | | | |
Db 1 FEDENFLL 8

RESULT 4

US-10-062-109A-328
; Sequence 328, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-328

Query Match 58.0%; Score 29; DB 14; Length 10;
Best Local Similarity 62.5%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
| | | | |
Db 3 RKPDPQHF 10

RESULT 5

US-10-005-480A-328
; Sequence 328, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-005-480A-328

Query Match 58.0%; Score 29; DB 14; Length 10;
Best Local Similarity 62.5%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
| | | | |
Db 3 RKPDPQHF 10

RESULT 6

US-09-880-748-2437

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; Sequence 2437, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2437
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2437
```

```
Query Match      58.0%; Score 29; DB 10; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 FPDENFKL 9
      |||:|:|
Db      7 FPDHSFSL 14
```

```
RESULT 7
US-09-880-748-2684
; Sequence 2684, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2684
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2684
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Query Match      58.0%; Score 29; DB 10; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 FPDENFKL 9
      |||:|:|
Db      7 FPDHSFSL 14
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RESULT 8

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US-10-293-418-2437
; Sequence 2437, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2437
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-2437
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```
Query Match      58.0%; Score 29; DB 12; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FPDENFKL 9
      |||:|:|
Db      7 FPDHSFSL 14
```

```
RESULT 9
US-10-293-418-2684
; Sequence 2684, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2684
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-2684
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Query Match 58.0%; Score 29; DB 12; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPPDENFKL 9
: : : : :
Db 7 FPDHSEFSL 14

RESULT 10

US-10-226-629A-464
; Sequence 464, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 464
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-464

Query Match 54.0%; Score 27; DB 14; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7
: : : : :
Db 1 KYPDLEF 7

RESULT 11

US-10-226-629A-477
; Sequence 477, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 477
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-477

Query Match 54.0%; Score 27; DB 14; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7
: : : : :
Db 2 KYPDLEF 8

RESULT 12
US-09-938-864-36
; Sequence 36, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-36

Query Match 54.0%; Score 27; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENFK 8
: : : : :
Db 2 QFPNHSFK 9

RESULT 13

US-09-791-477-36
; Sequence 36, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-36

Query Match 54.0%; Score 27; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENFK 8
: : : : :
Db 2 QFPNHSFK 9

RESULT 14

US-09-785-019-36
; Sequence 36, Application US/09785019
; Publication No. US20030082196A1

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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-785-019-36

Query Match          54.0%; Score 27; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 RFPDENFX 8
       :||: :||
Db      2 QFPNHSFX 9
```

```

RESULT 15
US-10-125-635A-36
; Sequence 36, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-125-635A-36
```

```

Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 RFPDENFX 8
       :||: :||
Db      2 QFPNHSFX 9
```

```

RESULT 16
US-10-002-603-36
; Sequence 36, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
```

```

; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-002-603-36
```

```

Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 RFPDENFX 8
       :||: :||
Db      2 QFPNHSFX 9
```

```

RESULT 17
US-10-062-109A-7
; Sequence 7, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-062-109A-7
```

```

Query Match          54.0%; Score 27; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 PDENFX 8
       :||: :||
Db      2 PDQHFX 7
```

```

RESULT 18
US-10-062-109A-560
; Sequence 560, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
```

```
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 560
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-560
```

```
Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 PDENFK 8
Db 2 PDQHRK 7
```

```
RESULT 19
US-10-226-629A-465
; Sequence 465, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 465
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-465
```

```
Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPPDENF 7
Db 1 KYPDLNF 7
```

```
RESULT 20
US-10-226-629A-478
; Sequence 478, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
```

```
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 478
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-478
```

```
Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPPDENF 7
Db 2 KYPDLNF 8
```

```
RESULT 21
US-10-226-629A-491
; Sequence 491, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 491
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-491
```

```
Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RPPDENF 7
Db 3 KYPDLNF 9
```

```
RESULT 22
US-10-005-480A-7
; Sequence 7, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
```

TYPE: PRT
ORGANISM: Homo Sapien
US-10-005-480A-7

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
Db 2 PDQHF 7

RESULT 23

US-10-005-480A-560
Sequence 560, Application US/10005480A
Publication No. US20030191073A1
GENERAL INFORMATION:
APPLICANT: Agnieszka
APPLICANT: Chalilta-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.00
CURRENT APPLICATION NUMBER: US/10/005,480A
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 560
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-005-480A-560

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
Db 2 PDQHF 7

RESULT 24

US-10-195-835-36
Sequence 36, Application US/10195835
Publication No. US20030198622A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Smithgall, Molly D.
APPLICANT: Carter, Darrick
APPLICANT: Cheever, Martin A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Sutherland, R. Alec
APPLICANT: Mossman, Sally P.
APPLICANT: Evans, Lawrence S.
APPLICANT: Swanson, Ryan M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C8
CURRENT APPLICATION NUMBER: US/10/195,835,
CURRENT FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien

US-10-195-835-36

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 9;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
Db 2 QFPNHSFK 9

RESULT 25

US-10-286-333-36
Sequence 36, Application US/10286333
Publication No. US20030215458A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: McNeill, Patricia D.
APPLICANT: Jaya, No. US20030215458A1a1e
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C10
CURRENT APPLICATION NUMBER: US/10/286,333
CURRENT FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-10-286-333-36

Query Match
Best Local Similarity 54.0%; Score 27; DB 15; Length 9;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
Db 2 QFPNHSFK 9

RESULT 26

US-10-244-830-36
Sequence 36, Application US/10244830
Publication No. US20030235557A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
FILE REFERENCE: 210121.465C9
CURRENT APPLICATION NUMBER: US/10/244,830
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 468
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-10-244-830-36

Query Match
Best Local Similarity 54.0%; Score 27; DB 15; Length 9;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
Db 2 QFPNHSFK 9

RESULT 27

US-10-427-717-36
Sequence 36, Application US/10427717

```
; Publication No. US20040018204A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20040018204A1a1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C11
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 508
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-427-717-36
```

```
Query Match      54.0%; Score 27; DB 15; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 RFPDENFK 8
:|:|:|
Db 2 QFPNHSFK 9

```
RESULT 28
US-10-648-780-36
; Sequence 36, Application US/10648780
; Publication No. US20040126362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/648,780
; CURRENT FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-648-780-36
```

```
Query Match      54.0%; Score 27; DB 16; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 RFPDENFK 8
:|:|:|
Db 2 QFPNHSFK 9

```
RESULT 29
US-10-062-109A-196
; Sequence 196, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
```

```
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-196
```

```
Query Match      54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 3 PDENFK 8
||:|:|
Db 2 PDQHF 7

```
RESULT 30
US-10-062-109A-427
; Sequence 427, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-427
```

```
Query Match      54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 3 PDENFK 8
||:|:|
Db 2 PDQHF 7

```
RESULT 31
US-10-062-109A-507
; Sequence 507, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
```



```
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 507
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-062-109A-507
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 PDENFX 8
        ||::||
Db       2 PDQHF 7
```

```
RESULT 32
US-10-062-109A-614
; Sequence 614, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Chalilita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-062-109A-614
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 PDENFX 8
        ||::||
Db       2 PDQHF 7
```

```
RESULT 33
US-10-226-629A-466
; Sequence 466, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
```

```
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 466
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
; US-10-226-629A-466
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 RFPDENF 7
        ::|||
Db       1 KYPDLNF 7
```

```
RESULT 34
US-10-226-629A-479
; Sequence 479, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
; US-10-226-629A-479
```

```
Query Match          54.0%; Score 27; DB 14; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 RFPDENF 7
        ::|||
Db       2 KYPDLNF 8
```

```
RESULT 35
US-10-226-629A-492
; Sequence 492, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 492
LENGTH: 10
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-492

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7
DB 3 KYPDLNF 9

RESULT 36
US-10-226-629A-505
Sequence 505, Application US/10226629A
Publication No. US20030166504A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavit, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
FILE REFERENCE: 5006.01
CURRENT APPLICATION NUMBER: US/10/226,629A
CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,182
NUMBER OF SEQ ID NOS: 736
SOFTWARE: PatentIn version 3.1
SEQ ID NO 505
LENGTH: 10
TYPE: PRT
ORGANISM: Variola virus
US-10-226-629A-505

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPPDENF 7
DB 4 KYPDLNF 10

RESULT 37
US-10-005-480A-196
Sequence 196, Application US/10005480A
Publication No. US20030191073A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 51158-20062.00
CURRENT APPLICATION NUMBER: US/10/005,480A
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 196
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-10-005-480A-196

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
DB 2 PDQHF 7

RESULT 38
US-10-005-480A-427
Sequence 427, Application US/10005480A
Publication No. US20030191073A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 51158-20062.00
CURRENT APPLICATION NUMBER: US/10/005,480A
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 427
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-10-005-480A-427

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
DB 2 PDQHF 7

RESULT 39
US-10-005-480A-507
Sequence 507, Application US/10005480A
Publication No. US20030191073A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 51158-20062.00
CURRENT APPLICATION NUMBER: US/10/005,480A
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 507
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-10-005-480A-507

Query Match
Best Local Similarity 54.0%; Score 27; DB 14; Length 10;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||:|
Db 2 PDQHF 7

RESULT 40

US-10-005-480A-614

; Sequence 614, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-614

Query Match 54.0%; Score 27; DB 14; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||:|
Db 2 PDQHF 7

RESULT 41

US-10-226-629A-467

; Sequence 467, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 467
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-467

Query Match 54.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENF 7
::|||
Db 1 KYPDLNF 7

RESULT 42

US-10-226-629A-480

; Sequence 480, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 480
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-480

Query Match 54.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENF 7
::|||
Db 2 KYPDLNF 8

RESULT 43

US-10-226-629A-493

; Sequence 493, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 493
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-493

Query Match 54.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENF 7
::|||
Db 3 KYPDLNF 9

RESULT 44

US-10-226-629A-506

; Sequence 506, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian

```
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 506
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-506
```

```
Query Match      54.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 RPPDENF 7
       :|||
Db      4 KYPDLNF 10
```

```
RESULT 45
US-10-226-629A-518
; Sequence 518, Application US/10226629A
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 518
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-518
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Query Match      54.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      1 RPPDENF 7
       :|||
Db      5 KYPDLNF 11
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Search completed: August 30, 2004, 11:04:59
Job time : 12.0068 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-7
Perfect score: 50
Sequence: 1 RFPDENFKL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	62.0	10	2	US-08-658-639-8
2	31	62.0	10	3	US-08-944-604-8
3	29	58.0	10	3	PCT-US93-08067-4
4	28	56.0	14	3	US-09-041-886-48
5	25	50.0	10	1	US-08-290-448A-2
6	25	50.0	10	1	US-08-290-448A-2
7	25	50.0	10	1	US-08-175-069A-2
8	25	50.0	10	4	US-08-461-939B-2
9	25	50.0	10	4	US-08-464-000-2
10	25	50.0	11	1	US-08-290-448A-34
11	25	50.0	11	1	US-08-290-448A-34
12	25	50.0	11	1	US-08-175-069A-34
13	25	50.0	11	4	US-08-461-939B-34
14	25	50.0	11	4	US-08-464-000-34
15	24	48.0	8	1	US-08-378-859-3
16	24	48.0	8	3	US-08-970-648-3
17	24	48.0	8	4	US-08-952-558-4
18	24	48.0	9	2	US-08-522-269B-6
19	24	48.0	9	3	US-09-294-923-6
20	24	48.0	9	3	US-08-960-780-59
21	24	48.0	9	3	US-09-073-898-59
22	24	48.0	9	4	US-09-341-982-21
23	24	48.0	9	4	US-09-850-351A-59
24	24	48.0	10	4	US-09-341-982-36
25	24	48.0	11	4	US-09-341-982-58
26	24	48.0	12	2	US-08-934-222-25
27	24	48.0	12	2	US-08-933-402-25

28	24	48.0	12	2	US-09-207-621-25	Sequence 25, Appl
29	24	48.0	12	2	US-08-532-818-25	Sequence 25, Appl
30	24	48.0	12	3	US-09-231-797-25	Sequence 25, Appl
31	24	48.0	12	3	US-08-934-224-25	Sequence 25, Appl
32	24	48.0	12	3	US-08-933-843-25	Sequence 25, Appl
33	24	48.0	12	3	US-08-934-223-25	Sequence 25, Appl
34	24	48.0	12	3	US-09-413-492-25	Sequence 25, Appl
35	23	46.0	9	1	US-08-615-181-91	Sequence 91, Appl
36	23	46.0	9	4	US-09-492-543-73	Sequence 73, Appl
37	23	46.0	9	4	US-09-492-543-101	Sequence 101, Appl
38	23	46.0	9	4	US-09-688-188B-113	Sequence 113, Appl
39	23	46.0	9	4	US-09-291-417D-113	Sequence 113, Appl
40	23	46.0	10	1	US-08-261-206A-10	Sequence 10, Appl
41	23	46.0	10	1	US-08-261-206A-31	Sequence 31, Appl
42	23	46.0	10	1	US-08-261-206A-35	Sequence 35, Appl
43	23	46.0	10	1	US-08-261-206A-39	Sequence 39, Appl
44	23	46.0	10	1	US-08-261-206A-43	Sequence 43, Appl
45	23	46.0	10	4	US-09-688-188B-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-08-658-639-8
Sequence 8, Application US/08658639
Patent No. 5914238

GENERAL INFORMATION:
APPLICANT: KEESSE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-DYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-658-639-8

Query Match 62.0%; Score 31; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.4;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RFPDENFKL 9
Db 1 KPDENFKL 9

RESULT 2
US-08-944-604-8
Sequence 8, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: KEESSE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-YUE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-944-604-8

Query Match
Best Local Similarity 62.0%; Score 31; DB 3; Length 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPDENFKL 9
Db 1 KPDENFIL 9

RESULT 3
PCT-US93-08067-4
Sequence 4, Application PC/TUS9308067
GENERAL INFORMATION:
APPLICANT: Silva, Robert F
APPLICANT: Reilly, John D
TITLE OF INVENTION: PORTABLE INTRON AS AN INSERTION VECTOR FOR
GENE INSERTION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004-2201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08067
FILING DATE: 27-AUG-1993
CLASSIFICATION:
CLASSIFICATION: 435/235
CLASSIFICATION: C12N 7/00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application No. 07/936,423
FILING DATE: 27-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Holman, John C.
REGISTRATION NUMBER: 22,769
REFERENCE/DOCKET NUMBER: Q43813PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08067-4

Query Match
Best Local Similarity 58.0%; Score 29; DB 5; Length 10;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 RPDENFK 8
Db 4 YPDENFK 10

RESULT 4
US-09-041-886-48
Sequence 48, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-041-886-48

Query Match 56.0%; Score 28; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFK 8
| | | | |
Db 2 DENFK 6

RESULT 5
US-08-290-448A-2
; Sequence 2, Application US/08290448A
; Patent No. 5676954

GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-290-448A-2

Query Match 50.0%; Score 25; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 6
US-08-290-448A-2
; Sequence 2, Application US/08290448A
; Patent No. 5698204
; GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-290-448A-2

Query Match 50.0%; Score 25; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 7
US-08-175-069A-2
; Sequence 2, Application US/08175069A
; Patent No. 5776761
; GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-175-069A-2

Query Match 50.0%; Score 25; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 8
US-08-461-939B-2
Sequence 2, Application US/08461939B
Patent No. 6335019
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods for Treating Sensitivity To A
TITLE OF INVENTION: Protein Allergen Using Peptides which include A T Cell Epitope
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-000-2

REFERENCE/DOCKET NUMBER: IMT-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-461-939B-2

Query Match 50.0%; Score 25; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 9
US-08-464-000-2
Sequence 2, Application US/08464000
Patent No. 6335020
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,000
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018CN2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-000-2

Query Match 50.0%; Score 25; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 10

US-08-290-448A-34
; Sequence 34, Application US/08290448A

; Patent No. 5676954

; GENERAL INFORMATION:

; APPLICANT: Rogers, Bruce

; APPLICANT: Klapper, David G.

; APPLICANT: Rafnar, Thorunn

; APPLICANT: Kuo, Mei-chang

; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/290,448A

; FILING DATE: August 15, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/529,951

; FILING DATE: May 29, 1990

; APPLICATION NUMBER: US 07/325,365

; FILING DATE: March 17, 1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandragouras

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: IMI-018CN

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-290-448A-34

Query Match 50.0%; Score 25; DB 1; Length 11;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 11

US-08-290-448A-34
; Sequence 34, Application US/08290448A

; Patent No. 5676954

; GENERAL INFORMATION:

; APPLICANT: Rogers, Bruce

; APPLICANT: Klapper, David G.

; APPLICANT: Rafnar, Thorunn

; APPLICANT: Kuo, Mei-chang

; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A

FILING DATE: August 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-290-448A-34

Query Match 50.0%; Score 25; DB 1; Length 11;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 12

US-08-175-069A-34
; Sequence 34, Application US/08175069A

; Patent No. 5776761

; GENERAL INFORMATION:

; APPLICANT: Rogers, Bruce

; APPLICANT: Klapper, David G.

; APPLICANT: Rafnar, Thorunn

; APPLICANT: Kuo, Mei-chang

; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/175,069A

FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-175-069A-34

Query Match 50.0%; Score 25; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 13

US-08-461-939B-34
Sequence 34, Application US/08461939B
Patent No. 6335019
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods for Treating Sensitivity To A
TITLE OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epitope
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-461-939B-34

Query Match 50.0%; Score 25; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 14

US-08-464-000-34
Sequence 34, Application US/08464000
Patent No. 6335020
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,000
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMT-018CND2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-000-34

Query Match 50.0%; Score 25; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PDENFK 8
| | | | |
Db 5 PWENFK 10

RESULT 15
US-08-378-859-3
; Sequence 3, Application US/08378859
; Patent No. 5728553
; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R
; APPLICANT: Sleep, Darrell
; APPLICANT: van Urk, Hendrik
; APPLICANT: Berzenko, Stephen
; APPLICANT: Woodrow, John R
; APPLICANT: Johnson, Richard A
; APPLICANT: Wood, Patricia C
; APPLICANT: Burton, Steven J
; APPLICANT: Quirk, Alan V
; TITLE OF INVENTION: High Purity Albumin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill, New Providence
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,859
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H8501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 771 6292
; TELEFAX: (908) 771 6159
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Peptide fragment of human serum albumin
US-08-378-859-3

Query Match 48.0%; Score 24; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFK 8
Db 4 EENFK 8

RESULT 16
US-08-970-648-3
; Sequence 3, Application US/08970648
; Patent No. 6034221
; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R
; APPLICANT: Sleep, Darrell
; APPLICANT: van Urk, Hendrik
; APPLICANT: Berzenko, Stephen

APPLICANT: Woodrow, John R
APPLICANT: Johnson, Richard A
APPLICANT: Wood, Patricia C
APPLICANT: Burton, Steven J
APPLICANT: Quirk, Alan V
TITLE OF INVENTION: High Purity Albumin
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The BOC Group, Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill, New Providence
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,648
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378,859
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24,864
REFERENCE/DOCKET NUMBER: 92H8501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 771 6292
TELEFAX: (908) 771 6159
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Peptide fragment of human serum albumin
US-08-970-648-3

Query Match 48.0%; Score 24; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFK 8
Db 4 EENFK 8

RESULT 17
US-08-952-558-4
; Sequence 4, Application US/08952558
; Patent No. 6638740
; GENERAL INFORMATION:
; APPLICANT: Goodey, Andrew R.
; APPLICANT: Sleep, Darrell
; APPLICANT: Berzenko, Stephen
; APPLICANT: Woodrow, John R.
; APPLICANT: Johnson, Richard A.
; TITLE OF INVENTION: PROCESS OF HIGH PURITY ALBUMIN PRODUCTION
; FILE REFERENCE: CE0111D US
; CURRENT APPLICATION NUMBER: US/08/952,558
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: PCT/GB96/00449
; PRIOR FILING DATE: 1996-02-29
; PRIOR APPLICATION NUMBER: 378,859

PRIOR FILING DATE: 1995-05-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-08-952-558-4

Query Match 48.0%; Score 24; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DENFK 8
Db 4 EENFK 8

RESULT 18
US-08-522-269B-6
Sequence 6, Application US/08522269B
Patent No. 5919690

GENERAL INFORMATION:
APPLICANT: Knap, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofod, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59196900 No. 59196900disk of No. 59196900th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,269B
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-522-269B-6

Query Match 48.0%; Score 24; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFPD 4
Db 3 RFPD 6

RESULT 19
US-09-294-923-6
Sequence 6, Application US/09294923

Patent No. 6197566

GENERAL INFORMATION:
APPLICANT: Knap, Inge Helmer
APPLICANT: Hjort, Carsten M.
APPLICANT: Halkier, Torben
APPLICANT: Kofod, Lene Venke
TITLE OF INVENTION: An Alpha-Galactosidase Enzyme
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61975660 No. 6197566disk of No. 6197566th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,923
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/522,269
FILING DATE: 12-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 37,125
REFERENCE/DOCKET NUMBER: 3935.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-294-923-6

Query Match 48.0%; Score 24; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFPD 4
Db 3 RFPD 6

RESULT 20
US-08-960-780-59
Sequence 59, Application US/08960780
Patent No. 6204435

GENERAL INFORMATION:

APPLICANT: Feltelson, Jerald S.
APPLICANT: Schepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
SEQUENCES Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville

STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-960-780-59

Query Match 48.0%; Score 24; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6
Db 1 PDEN 4

RESULT 21
US-09-073-898-59
Sequence 59, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Feltelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstad-lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-073-898-59

Query Match 48.0%; Score 24; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDEN 6
Db 1 PDEN 4

RESULT 22
US-09-341-982-21
Sequence 21, Application US/09341982
Patent No. 6558671
GENERAL INFORMATION:
APPLICANT: SLINGLUFF, Craig L.
APPLICANT: HUNT, Donald F.
APPLICANT: ENGELHARD, Victor H.
APPLICANT: KITTELSEN, David
TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
FILE REFERENCE: SLINGLUFF=3B
CURRENT APPLICATION NUMBER: US/09/341,982
CURRENT FILING DATE: 1999-09-20
EARLIER APPLICATION NUMBER: PCT/US98/01592
EARLIER FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: 60/037,781
EARLIER FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Fragment of
OTHER INFORMATION: human protein
US-09-341-982-21

Query Match 48.0%; Score 24; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
Db 2 DENFTI 7

RESULT 23
US-09-850-351A-59

; Sequence 59, Application US/09850351A
; Patent No. 6656908
; GENERAL INFORMATION:
; APPLICANT: Feltelson, Jerald S.
; Schnepf, H. Ernest
; Narva, Kenneth E.
; Stockhoff, Brian A.
; Schmelts, James
; Loewer, David
; Dullum, Charles Joseph
; Muller-Cohn, Judy
; Stamp, Lisa
; Morrill, George
; TITLE OF INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide
; Sequences Which Encode These Toxins
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,351A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/073,898
; FILING DATE: 06-May-1998
; APPLICATION NUMBER: US 08/960,780
; FILING DATE: 30-OCT-1997
; APPLICATION NUMBER: US 60/029,848
; FILING DATE: 30-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-708CD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-850-351A-59
Query Match 48.0%; Score 24; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PDEN 6
Db 1 PDEN 4
RESULT 24
US-09-341-982-36
; Sequence 36, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.

; APPLICANT: KITTESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-36

Query Match 48.0%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
Db 3 DENFTI 8

RESULT 25
US-09-341-982-58
; Sequence 58, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-58

Query Match 48.0%; Score 24; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DENFKL 9
Db 4 DENFTI 9

RESULT 26
US-08-934-222-25
; Sequence 25, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-25

Query Match 48.0%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||:|:
Db 5 PDDDR 10

RESULT 27
US-08-933-402-25
Sequence 25, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-402-25

Query Match 48.0%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||:|:
Db 5 PDDDR 10

RESULT 28
US-09-207-621-25
Sequence 25, Application US/09207621
Patent No. 5952465
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction S:
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-207-621-25

Query Match 48.0%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
|::|:
Db 5 PDDDFR 10

RESULT 29

US-08-532-818-25
Sequence 25, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-25

Query Match 48.0%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
|::|:
Db 5 PDDDFR 10

RESULT 30
US-09-231-797-25
Sequence 25, Application US/09231797

Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-25

Query Match 48.0%; Score 24; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
|::|:
Db 5 PDDDFR 10

RESULT 31
US-08-934-224-25
Sequence 25, Application US/08934224
Patent No. 6100044
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-25

Query Match 48.0%; Score 24; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||::||:
Db 5 PDDDFR 10

RESULT 32
US-08-933-843-25
Sequence 25, Application US/08933843
Patent No. 611069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:

NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-843-25

Query Match 48.0%; Score 24; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||::||:
Db 5 PDDDFR 10

RESULT 33
US-08-934-223-25
Sequence 25, Application US/08934223
Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-25

Query Match 48.0%; Score 24; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PDENFK 8
||::||:
Db 5 PDDDFR 10

Db 5 PDDDFR 10

RESULT 34

US-09-413-492-25
; Sequence 25, Application US/09413492
; Patent No. 6258550

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-413-492-25

Query Match 48.0%; Score 24; DB 3; Length 12;

Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;QY 3 PDENFK 8
|:|:|:

Db 5 PDDDFR 10

RESULT 35

US-08-615-181-91
; Sequence 91, Application US/08615181
; Patent No. 5756666

GENERAL INFORMATION:

APPLICANT: MASAFUMI, TAKIGUCHI
APPLICANT: MIWA, KIYOSHI
TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
TITLE OF INVENTION: CURING AIDS
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VACOUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,181
FILING DATE: 04-APR-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/01756
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261302/1993
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-796-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-91

Query Match 46.0%; Score 23; DB 1; Length 9;

Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;QY 3 PDENFK 8
|:|:|:

Db 3 PEESEFR 8

RESULT 36

US-09-492-543-73
; Sequence 73, Application US/09492543A
; Patent No. 6316213
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-B
CURRENT APPLICATION NUMBER: US/09/492,543A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 189
SOFTWARE: WORD 6.0.1 for Macintosh
SEQ ID NO 73
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-09-492-543-73Query Match 46.0%; Score 23; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;QY 3 PDENFK 8
|:|:|:

Db 3 PEESEFR 8

RESULT 36

US-09-492-543-73
; Sequence 73, Application US/09492543A
; Patent No. 6316213
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-B
CURRENT APPLICATION NUMBER: US/09/492,543A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 189
SOFTWARE: WORD 6.0.1 for Macintosh
SEQ ID NO 73
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-09-492-543-73

Query Match 46.0%; Score 23; DB 4; Length 9;

Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;QY 3 PDENFK 8
|:|:|:

Db 3 PEESEFR 8

RESULT 36

US-09-492-543-73
; Sequence 73, Application US/09492543A
; Patent No. 6316213
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
FILE REFERENCE: D6223CIP-B
CURRENT APPLICATION NUMBER: US/09/492,543A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 189
SOFTWARE: WORD 6.0.1 for Macintosh
SEQ ID NO 73
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-09-492-543-73Query Match 46.0%; Score 23; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENFKL 9
:||||
Db 5 QNFKL 9

RESULT 37

US-09-492-543-101
; Sequence 101, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B
; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-09-492-543-101

Query Match 46.0%; Score 23; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENFKL 9
:||||
Db 5 QNFKL 9

RESULT 38
US-09-688-188B-113
; Sequence 113, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WAYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-113

Query Match 46.0%; Score 23; DB 4; Length 9;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFK 8
|||:::
Db 3 FPKEDYR 9

RESULT 39

US-09-291-417D-113
; Sequence 113, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WAYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-113

Query Match 46.0%; Score 23; DB 4; Length 9;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFK 8
|||:::
Db 3 FPKEDYR 9

RESULT 40
US-08-261-206A-10
; Sequence 10, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-206A-10

Query Match 46.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8
|||
|:
Db 4 FPDPCFR 10

RESULT 41

US-08-261-206A-31
; Sequence 31, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-261-206A-31

Query Match 46.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8
|||
|:
Db 4 FPDPCFR 10

RESULT 42

US-08-261-206A-35

; Sequence 35, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-261-206A-35

Query Match 46.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFK 8
|||
|:
Db 4 FPDPCFR 10

RESULT 43

US-08-261-206A-39
; Sequence 39, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia

COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-206A-39

Query Match 46.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFX 8
DB 4 FPDPCFR 10

RESULT 44
US-08-261-206A-43
Sequence 43, Application US/08261206A
Patent No. 5574007
GENERAL INFORMATION:
APPLICANT: Zushi, Mitichitaka
APPLICANT: Gomi, Komakazu
APPLICANT: Yamamoto, Shuji
APPLICANT: Suzuki, Koji
APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-206A-43

Query Match 46.0%; Score 23; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFX 8
DB 4 FPDPCFR 10

RESULT 45
US-09-688-188B-79
Sequence 79, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHITE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 79
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-688-188B-79

Query Match 46.0%; Score 23; DB 4; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFX 8
DB 4 FPKEDYR 10

Search completed: August 30, 2004, 10:57:17
Job time : 4.55743 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4088 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-7
Perfect score: 50
Sequence: 1 RFPDENFKL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	50	100.0	9	3	AAy69927	AAy69927 Human cyc
2	41	82.0	11	3	AAy69926	AAy69926 Human cyc
3	32	64.0	10	7	ADA06843	Ada06843 Solid pha
4	31	62.0	10	2	AAW44362	Aaw44362 Breast ca
5	31	62.0	10	4	AAB98714	Aab98714 Human bre
6	30	60.0	9	6	ABR58800	Abri58800 Alzheimer
7	29	58.0	9	4	AAU68482	Aau68482 Human Bre
8	29	58.0	9	5	ABG67487	Abg67487 Human ADP
9	29	58.0	9	6	ADA23600	Ada23600 Alzheimer
10	29	58.0	9	7	ABR62869	Abri62869 Tumourige
11	29	58.0	9	7	ADE66799	Ade66799 Human 161
12	29	58.0	9	7	ADE68459	Ade68459 Human 161
13	29	58.0	9	7	ADE68822	Ade68822 Human 161
14	29	58.0	10	2	AAr49843	Aar49843 GB fragme
15	29	58.0	10	7	ADE69600	Ade69600 Human 161
16	29	58.0	10	7	ADE66863	Ade66863 Human 161
17	29	58.0	10	7	ADE69184	Ade69184 Human 161
18	29	58.0	10	7	ADE66681	Ade66681 Human 161
19	29	58.0	10	7	ADE69916	Ade69916 Human 161
20	29	58.0	13	5	AAU69665	Aau69665 Cell deat
21	29	58.0	14	5	ABP46673	Abp46673 Human Bly
22	29	58.0	14	5	ABP46426	Abp46426 Human Bly
23	28	56.0	9	6	ABJ42183	Abj42183 151P3D4 C
24	28	56.0	9	6	ABJ41418	Abj41418 151P3D4 C
25	28	56.0	9	6	ABJ44334	Abj44334 151P3D4 C

26	28	56.0	9	6	ABJ45672	Abj45672 151P3D4 C
27	28	56.0	9	6	ABJ47747	Abj47747 151P3D4 C
28	28	56.0	9	6	ABJ49116	Abj49116 151P3D4 C
29	28	56.0	9	6	ABJ41779	Abj41779 151P3D4 C
30	28	56.0	9	6	ABJ41872	Abj41872 151P3D4 C
31	28	56.0	9	6	ABJ47004	Abj47004 151P3D4 C
32	28	56.0	9	6	ABJ39404	Abj39404 151P3D4 C
33	28	56.0	9	6	ABJ44281	Abj44281 151P3D4 C
34	28	56.0	9	6	ABJ45005	Abj45005 151P3D4 C
35	28	56.0	9	6	ABJ45032	Abj45032 151P3D4 C
36	28	56.0	9	6	ABJ48393	Abj48393 151P3D4 C
37	28	56.0	9	6	ABJ43122	Abj43122 151P3D4 C
38	28	56.0	9	6	ABJ46322	Abj46322 151P3D4 C
39	28	56.0	9	6	ABJ47111	Abj47111 151P3D4 C
40	28	56.0	9	6	ABJ48392	Abj48392 151P3D4 C
41	28	56.0	9	6	ABJ39852	Abj39852 151P3D4 C
42	28	56.0	9	6	ABJ41450	Abj41450 151P3D4 C
43	28	56.0	9	6	ABJ46607	Abj46607 151P3D4 C
44	28	56.0	9	6	ABJ40977	Abj40977 151P3D4 C
45	28	56.0	9	6	ABJ49160	Abj49160 151P3D4 C

ALIGNMENTS

RESULT 1

AAy69927 standard; peptide; 9 AA.

11-APR-2000 (first entry)

Human cyclophilin B peptide fragment #7.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
HLA antigen; diagnosis; tumour; therapy.

Homo sapiens.

WO9967288-A1.

29-DEC-1999.

24-JUN-1999; 99WO-JP003360.

25-JUN-1998; 98JP-00178449.

(SUMU) SUMITOMO PHARM CO LTD.

(ITOH/) ITOH K.

Itch K, Gomi S;

WPI; 2000-116932/10.

Tumour antigen peptides derived from cyclophilin B for treatment and
diagnosis of tumors.

Claim 4; Page 51; 64pp; Japanese.

This sequence represents a cyclophilin B peptide of the invention. The
peptides are tumour antigen peptides derived from cyclophilin B, that
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
peptides are used for the treatment and diagnosis of tumours

Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFPDENFKL 9
|||||

Db 1 RPPDENFKL 9

RESULT 2
AAV69926
ID AAV69926 standard; peptide; 11 AA.
XX
AC AAV69926;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #6.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 50; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;

Query Match 82.0%; Score 41; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPDENF 7
Db 5 RPPDENF 11

RESULT 3
ADA06843
ID ADA06843 standard; peptide; 10 AA.
XX
AC ADA06843;
XX
DT 06-NOV-2003 (first entry)
XX
DE Solid-phase synthesis produced organic peptide #5.
XX
KW Aldehyde functionalised support material; solid-phase synthesis;
KW organic compound; acid; thioacid; thioester; alcohol;
KW disubstituted amide; aldehyde.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER

FT /note= "OTHER= "Fmoc-Arg"
FT Misc-difference 2 /note= "D-form residue"
FT FT Modified-site 10 /label= OTHER
FT FT /note= "OTHER= "Ala-OAl"
XX
PN US6566494-B1.
XX
PD 20-MAY-2003.
XX
PF 11-MAY-1999; 99US-00309828.
XX
PR 18-JUN-1996; 96US-00665509.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Jensen KJ, Barany G, Songster MF, Albericio F, Alsina J;
PI Vagner J;
XX
DR WPI; 2003-596202/56.
XX
PT New aldehyde functionalized support material used for solid phase organic
PT synthesis.
XX
PS Example 14; Col 18; 18pp; English.
XX
CC The invention is related to an aldehyde functionalised support material.
CC The aldehyde functionalised support material is used for solid-phase
CC synthesis of organic compounds, particularly peptides. The organic
CC compounds can have a variety of C-terminal functionalities e.g. acids,
CC thioacids, thioesters, alcohols, disubstituted amides and aldehydes can
CC be produced. This sequence represents an organic peptide prepared by
CC solid-phase synthesis, using the support material of the invention.
XX
SQ Sequence 10 AA;

Query Match 64.0%; Score 32; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPDENFK 8
Db 1 RPPEDNYE 8

RESULT 4
AAW44362
ID AAW44362 standard; peptide; 10 AA.
XX
AC AAW44362;
XX
DT 28-MAY-1998 (first entry)
XX
DE Breast cancer-associated protein fragment BC-8 SEQ ID NO:8.
XX
KW Human; breast cancer-associated protein; nuclear matrix protein;
KW detection; diagnosis; antibody.
XX
OS Homo sapiens.
XX
PN WO9746884-A1.
XX
PD 11-DEC-1997.
XX
PF 03-JUN-1997; 97WO-US009529.
XX
PR 05-JUN-1996; 96US-00658639.
XX
PA (MATR-) MATRITECH INC.
XX
PI Keesee SK, Obar R, Wu Y;
XX

DR WPI; 1998-042336/04.
XX
PT Diagnosing breast cancer by detecting a breast cancer-associated protein
PT - allows early and reliable diagnosis and treatment monitoring, and
PT antibody or inhibitory compounds useful for treating breast cancer.
XX
PS Claim 10; Page 30; 47pp; English.
XX
PS The present sequence represents a breast cancer-associated protein
CC fragment for use in a method for diagnosing breast cancer in tissue or
CC body fluid by detecting one or more breast cancer-associated protein(s).
CC Alternatively a nucleic acid encoding a breast cancer-associated protein
CC is detected in the sample by the use of a nucleic acid probe. The breast
CC cancer-associated proteins, encoding nucleic acids and antibodies are
CC useful in diagnostic assays and kits for breast cancer detection. The
CC proteins are also useful in screening for inhibitory compounds and
CC monitoring effectiveness of treatments. The antibody, or pharmaceutical
CC compositions containing the antibody or the inhibitory compound, can be
CC administered to patients to treat breast cancer. The methods allow
CC reliable and early diagnosis of breast cancer, or prediction of its
CC onset, by detection of specific markers expressed in breast tumour cells
CC but not in non-cancerous breast cells
XX
SQ Sequence 10 AA;
SQ
Query Match 62.0%; Score 31; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPPDENFKL 9
: |||||
Db 1 KPDDENFIL 9
:
RESULT 5
AAB98714
ID AAB98714 standard; peptide; 10 AA.
XX
AC AAB98714;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human breast cancer-associated protein BC-8 peptide, SEQ ID NO:8.
XX
KW Human breast cancer-associated protein; BC-8; marker protein;
KW nuclear matrix protein; diagnosis; detection; tumour.
XX
OS Homo sapiens.
XX
PN US6218131-B1.
XX
PD 17-APR-2001.
XX
PF 06-OCT-1997; 97US-00944604.
XX
PR 05-JUN-1996; 96US-00658639.
XX
PA (MATR-) MATRITECH INC.
XX
PI Keesee SK, Obar R, Wu Y;
XX
DR WPI; 2001-396355/42.
XX
PT Diagnosing or detecting breast cancer in an individual comprises
PT detecting the presence of breast cancer-associated proteins in a
PT biological sample.
XX
PS Claim 9; Col 8; 30pp; English.
XX
PS The invention relates to novel human breast cancer-associated proteins,
CC and their use in diagnosing and detecting breast cancer. The breast
CC cancer-associated proteins of the invention are nuclear matrix proteins
CC designated BC-2 (AAB98720), BC-8 isoform A (BC-8A, AAB98721) and CC BC-8

CC isoform B (BC-8B, AAB98722), although 6 other breast cancer-associated
CC nuclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were
CC also isolated (sequences not given in the specification). The novel
CC breast cancer-associated proteins are present in the nuclear matrix of
CC breast cancer cells, but are not present in the nuclear matrix of cells
CC from normal breast tissue. The invention also encompasses fragments of
CC the breast cancer-associated proteins (AAB98709-AAB98716), and methods
CC for their use in breast cancer diagnosis. The breast cancer marker
CC proteins of the invention or fragments thereof may be detected in a
CC sample of breast tissue or blood from an individual. Isolated breast
CC cancer-associated proteins may also be used to prepare antibodies,
CC particularly monoclonal antibodies, which may be used to detect or
CC diagnose breast cancer. Nucleic acids encoding the breast cancer-
CC associated proteins may also be used in the diagnosis and detection of
CC breast cancer, and in the isolation of DNA or protein sequences which may
CC interact with breast cancer-associated nuclear matrix proteins. Sequences
CC AAB98712-AAB98716 represent specifically claimed fragments of breast
CC cancer-associated protein BC-8
XX
SQ Sequence 10 AA;
SQ
Query Match 62.0%; Score 31; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPPDENFKL 9
: |||||
Db 1 KPDDENFIL 9
:
RESULT 6
ABR58800
ID ABR58800 standard; peptide; 9 AA.
XX
AC ABR58800;
XX
DT 11-JUL-2003 (first entry)
XX
DE Alzheimer's Disease-associated protein isoform, APL-333, SEQ ID 118.
XX
KW Nootropic; Neuroprotective; Alzheimer's disease; API; human;
KW Alzheimer's Disease-associated protein isoform.
XX
OS Homo sapiens.
XX
PN WO2003028543-A2.
XX
PD 10-APR-2003.
XX
PF 03-OCT-2002; 2002WO-US031642.
XX
PR 03-OCT-2001; 2001US-0326708P.
XX
PA (Pfizer) Pfizer Prod Inc.
XX (Oxford) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Durham LK, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Snyder PU, Soares HD, Stiger TR;
PI Sunderland PT, Townsend RR, White WF, Williams SA;
XX
DR WPI; 2003-371957/35.
XX
PT Screening or diagnosing of Alzheimer's disease (AD) determine the stage
PT or severity of AD in a subject, comprises analyzing a test sample of body
PT fluid from the subject by 2-dimensional electrophoresis.
XX
PS Claim 2; Page 34; 179pp; English.
XX
PS The present invention relates to methods for screening or diagnosing
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a
CC subject, to identify subject at risk of developing AD, or to monitor the
CC effect of therapy administered. The methods comprise analysing a test
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-

CC dimensional array of AD-associated features (AFs). The method
CC alternatively comprises quantitatively detecting in a sample of body
CC fluid from the subject, one or more AD-associated protein isoforms (APIs;
CC ABR58710-ABR59184)
XX
SQ Sequence 9 AA;

Query Match 60.0%; Score 30; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
DB 1 FEDENFLL 8

RESULT 7
AAU68482
ID AAU68482 standard; peptide; 9 AA.

AC AAU68482;
XX
DT 16-JAN-2002 (first entry)

DE Human Breast cancer-associated protein isoform, BPI-270 peptide #2.

KW Human; Breast cancer-associated protein isoform; breast cancer;
KW Immunogen; cytostatic; BPI; tryptic digest peptide.

OS Homo sapiens.

PN WO200171357-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-GB001219.

PR 20-MAR-2000; 2000GB-00006695.
PR 24-MAR-2000; 2000GB-00007265.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

PS WPI; 2001-611532/70.

PT Identifying proteins for clinical screening, diagnosis and prognosis of
PT breast cancer, comprises detecting Breast Cancer-Associated Protein
PT Isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 53; 197pp; English.

CC The invention relates to diagnosing, determining the stage or severity,
CC or identifying the risk of a subject developing cancer (especially breast
CC cancer), or monitoring the effect of therapy on a subject with cancer,
CC comprising analysing a test sample using two-dimensional electrophoresis
CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
CC methods disclosed are used for the diagnosis and prognosis of breast
CC cancer, for determining the severity of breast cancer, and for
CC identifying a subject at risk of developing breast cancer, and monitoring
CC the effect of therapy administered to a subject. Antibodies raised
CC against the binding domain of a BPI, the binding domain of a BPI, a
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
CC of a BPI can be incorporated into a pharmaceutical composition for
CC treating or preventing breast cancer. The methods use sensitive and
CC specific biomarkers provide early diagnosis of breast cancer, and the
CC compositions are more potent, specific, and has a more rapid effect with
CC fewer side effects than other prior art methods. The present sequence is
CC a tryptic digest peptide from a BPI of the invention
XX
SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 4; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
DB 1 FEDENFLL 8

RESULT 8
ABG67487
ID ABG67487 standard; peptide; 9 AA.

AC ABG67487;
XX

DT 07-OCT-2002 (first entry)

DE Human ADPI tryptic digest peptide #196.

KW Human; Alzheimer's disease; AD; brain tissue; ADPI; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.

OS Homo sapiens.

PN WO200246767-A2.

PD 13-JUN-2002.

PF 29-NOV-2001; 2001WO-GB005289.

PR 08-DEC-2000; 2000US-0254431P.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMC, Parekh RB, Rohlf C;

PS WPI; 2002-508575/54.

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.

PS Claim 7; Page 72; 427pp; English.

CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides
XX
SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
DB 1 FEDENFLL 8

Db 1 FEDENFTL 8

RESULT 9
ADA23600
ID ADA23600 standard; peptide; 9 AA.

XX AC ADA23600;

XX DT 20-NOV-2003 (first entry)

XX DE Alzheimer's disease-associated protein isoform tryptic peptide #209.

XX KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
XX KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
XX KW Alzheimer's disease-associated protein isoform; ADPI.

XX OS Homo sapiens.

XX PN US2003064411-A1.

XX PD 03-APR-2003.

XX PF 10-DEC-2001; 2001US-00014340.

XX PR 08-DEC-2000; 2000US-0254431P.

XX PA (HERA/) HERATH H M A C.

XX PA (PARE/) PAREKH R B.

XX PA (ROHL/) ROHLFF C;

XX PI Herath HMA, Parekh RB, Rohlf C;

XX DR WPI; 2003-540784/51.

XX PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
XX PT involves analyzing test sample of brain tissue from subject, and
XX PT comparing feature in test sample with that of person(s) free from
XX PT Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 209; 115pp; English.

XX CC The invention relates to a method of screening or diagnosing Alzheimer's
XX CC disease in a subject. The method is useful for screening, diagnosis or
XX CC prognosis of Alzheimer's disease in a subject for determining the stage
XX CC of severity of Alzheimer's disease in a subject, for identifying a
XX CC subject at risk of developing Alzheimer's disease, or for monitoring the
XX CC effect of therapy administered to a subject having Alzheimer's disease.
XX CC The method is also useful in treating vascular dementia, Lewy body
XX CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
XX CC depression. The inventive method identifies sensitive and specific
XX CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
XX CC It provides therapeutic agents for Alzheimer's disease that works
XX CC quickly, potentially, specifically with fewer side effects. The present
XX CC sequence represents the amino acid sequence of a Alzheimer's disease-
XX CC associated protein isoform tryptic peptide.

XX SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFTL 9
Db 1 FEDENFTL 8

RESULT 10
ABR62869
ID ABR62869 standard; peptide; 9 AA.
XX ABR62869;

XX DT 04-DEC-2003 (first entry)

XX DE Tumourigenesis, metastasis-associated T cell cyclophilin peptide.

XX KW Cyclophilin; peptidyl-prolyl cis-trans isomerase; enzyme; tumourigenesis;
XX KW metastasis; cancer; diagnosis; human.

XX OS Homo sapiens.

XX PN WO2003060522-A1.

XX PD 24-JUL-2003.

XX PF 28-DEC-2002; 2002WO-KR002469.

XX PR 29-DEC-2001; 2001KR-00088090.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.

XX PI KO JH, Hwang SY, Sohn H, Oh S, Lee JH, Lee SC, Yoo J, Lee D;

XX DR WPI; 2003-646050/61.

XX PT Diagnosing cancers by measuring the changes of N-linked sugar chains of
XX PT proteins related to tumorigenesis and metastasis, including cancers of
XX PT the large intestine, stomach, lung, liver, uterus, breast and pancreas.

XX PS Example 3; Page 42; 49pp; English.

XX CC The present sequence is a peptide fragment of T cell cyclophilin
XX CC (peptidyl-prolyl cis-trans isomerase). Changes in glycosylation of this
XX CC protein are associated with metastasis and tumourigenesis. The protein
XX CC has 3 preserved N-linked sugar chain sites. A method for diagnosing
XX CC cancer involves measuring changes of sugar chains of proteins related to
XX CC tumorigenesis and metastasis. The changes are especially changes of sugar
XX CC chain branches of N-linked beta-1,6 N-acetylglucosamine. The protein is
XX CC prostate-derived factor, peptidyl-prolyl cis-trans isomerase, galectin
XX CC binding protein, L3 antigen, Mac-2-binding protein, serum protein 90K,
XX CC tumour associated antigen 90K, TIMP-1 and a novel, unidentified protein.
XX CC The cancer is large intestine cancer, stomach cancer, lung cancer, liver
XX CC cancer, uterine cancer, breast cancer and pancreas cancer

XX SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFTL 9
Db 1 FEDENFTL 8

RESULT 11
ADE66799
ID ADE66799 standard; peptide; 9 AA.
XX AC ADE66799;
XX DT 29-JAN-2004 (first entry)
XX DE Human 161P2F10B protein-related peptide 806.
XX KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX OS Homo sapiens.
XX PN WO2003040340-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US036002.

XX 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eld PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 151; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 58.0%; Score 29; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RFPDENFK 8
DB 2 RKPDQHF 9
XX
RESULT 12
ADE68459
ID ADE68459 standard; peptide; 9 AA.
XX
AC ADE68459;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2464.
XX
KM 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eld PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides

PT and polypeptides.
XX
PS Claim 13; Page 164; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 58.0%; Score 29; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RFPDENFK 8
DB 2 RKPDQHF 9
XX
RESULT 13
ADE68822
ID ADE68822 standard; peptide; 9 AA.
XX
AC ADE68822;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 2827.
XX
KM 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eld PM;
XX
DR WPI; 2003-441560/41.
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
PS Claim 13; Page 166; 135pp; English.
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid

CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX
SQ Sequence 9 AA;

Query Match 58.0%; Score 29; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RFPDENFK 8
| | | | |
| | | | |
Db 2 RKPDQHF 9

RESULT 14

AAR49843
ID AAR49843 standard; protein; 10 AA.

XX
AC AAR49843;

XX
DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 18-OCT-1994 (first entry)

XX
DE GB fragment corresp. to EcoRV site area.

XX
KM Type A; type B; portable intron; Marek's disease virus; MDV; B antigen;

KW A antigen; pin(E/K); pin(P/P); exon.

XX
OS Marek disease virus type 1.

XX
PN WO9405784-A1.

XX
PD 17-MAR-1994.

XX
PF 27-AUG-1993; 93WO-US008067.

XX
PR 27-AUG-1992; 92US-00936423.

XX
PA (USDA) US SEC OF AGRIC.

XX
PI Reilly JD, Silva RF;

XX
DR WPI; 1994-101189/12.

DR N-PSDB; AAQ44505.

XX
PT Portable intron for use as a vector for gene insertion - can be used to
PT express foreign genes in a host or correct defects in the host's
PT expression of a gene.

XX
PS Example 5; Fig 12A; 88pp; English.

XX
CC Example 5 describes the insertion of type A portable intron into B

CC antigen gene. AAQ44505 comprises the coding sequence surrounding the

CC EcoRV site in gB. AAQ44506 comprises the coding sequence after the

CC inserted type A portable intron is spliced out of gB. The amino acids

CC contributed by the type A portable intron exon sequences remain in gB

CC after RNA splicing. The translational reading frame is not disrupted.

CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to

CC correct OS field.)

XX
SQ Sequence 10 AA;

Query Match 58.0%; Score 29; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 FPDENFK 8
: | : | : |
: | : | : |
Db 4 YPQDNFK 10

RESULT 15

ADE69600

ID ADE69600 standard; peptide; 10 AA.

XX
AC ADE69600;

XX
DT 29-JAN-2004 (first entry)

XX
DE Human 161P2F10B protein-related peptide 3605.

XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX
OS Homo sapiens.

XX
PN WO2003040340-A2.

XX
PD 15-MAY-2003.

XX
PF 07-NOV-2002; 2002WO-US036002.

XX
PR 07-NOV-2001; 2001US-00005480.

PR 31-JAN-2002; 2002US-00062109.

XX
PA (AGEN-) AGENSYS INC.

XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;

PI Morrison RK, Chailita-Eid PM;

XX
DR WPI; 2003-441560/41.

XX
PT A composition for diagnosing, preventing and treating cancer (e.g.

PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides

PT and polypeptides.

XX
PS Claim 13; Page 171; 135pp; English.

XX
CC This invention relates to a novel composition which comprises a substance

CC that modulates the status of a novel human protein (161P2F10B) and its

CC variants having a sequence of 875 amino acids provided in the

CC specification. The protein of the invention is over-expressed in certain

CC cancers. The compounds of the invention may have cytostatic activity and

CC be useful for gene therapy or the development of a vaccine. The

CC composition and methods of the invention are useful in diagnosing,

CC preventing and treating cancer. The present sequence is the amino acid

CC sequence of a peptide which is derived from the sequence of the human

CC 161P2F10B protein and which may be used in the development of the

CC compounds of the invention.

XX
SQ Sequence 10 AA;

Query Match 58.0%; Score 29; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RFPDENFK 8
| | | | |
| | | | |
Db 3 RKPDQHF 10

XX
ID ADE66863 standard; peptide; 10 AA.

XX
AC ADE66863;

XX
DT 29-JAN-2004 (first entry)

XX
DE Human 161P2F10B protein-related peptide 870.

XX
KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX
OS Homo sapiens.

XX WO2003040340-A2.
PN 15-MAY-2003.
XX 07-NOV-2002; 2002WO-US036002.
PF 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX (AGEN-) AGENSYS INC.
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
DR A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX Claim 13; Page 152; 135pp; English.
PS
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
Query Match 58.0%; Score 29; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPPDENFK 8
Db 3 RKPQHF 10
RESULT 17
ADE69184
ID ADE69184 standard; peptide; 10 AA.
XX
AC ADE69184;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 3189.
XX
XM 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;

PI Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX Claim 13; Page 169; 135pp; English.
PS
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 10 AA;
Query Match 58.0%; Score 29; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPPDENFK 8
Db 1 RKPQHF 8
RESULT 18
ADE66681
ID ADE66681 standard; peptide; 10 AA.
XX
AC ADE66681;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 161P2F10B protein-related peptide 688.
XX
XM 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003040340-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US036002.
XX
PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
PI Morrison RK, Challita-Eid PM;
XX WPI; 2003-441560/41.
XX
PF A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX Claim 13; Page 150; 135pp; English.
PS
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the

CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX
SQ Sequence 10 AA;

Query Match 58.0%; Score 29; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
| | | | |
| | | | |
Db 3 RKPQHF 10

RESULT 19
ADE69916
ID ADE69916 standard; peptide; 10 AA.

AC ADE69916;

DT 29-JAN-2004 (first entry)

DE Human 161P2F10B protein-related peptide 3921.

KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

OS Homo sapiens.

PN WO2003040340-A2.

PD 15-MAY-2003.

PF 07-NOV-2002; 2002WO-US036002.

PR 07-NOV-2001; 2001US-00005480.

PR 31-JAN-2002; 2002US-00062109.

PA (AGEN-) AGENSYS INC.

PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;

PI Morrison RK, Challita-Eid PM;

DR WPI; 2003-441560/41.

PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.

PS Claim 13; Page 174; 135pp; English.

XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.

XX Sequence 10 AA;

Query Match 58.0%; Score 29; DB 7; Length 10;

Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFPDENFK 8
| | | | |
| | | | |
Db 1 RKPQHF 8

RESULT 20
AAU69665

ID AAU69665 standard; protein; 13 AA.

AC AAU69665;

DT 30-JAN-2002 (first entry)

DE Cell death protective sequence CNI-00727, protein #18.

KW Human; protective sequence; cell death; cerebral oedema; infection;
KW meningitis; degenerative disease; Alzheimer's disease; heart disease;
KW motor neuron disease; demyelinating disease; multiple sclerosis; asthma;
KW nutritional condition; peripheral nervous system disorder; ischaemia;
KW diabetic neuropathy; autoimmune haemolytic anaemia; respiratory system;
KW oral cavity; gastrointestinal tract; liver; cirrhosis; pancreatitis;
KW polycystic renal disease; urinary tract; genitalia; endometriosis;
KW breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis;
KW adrenal gland; skin; psoriasis; muscular atrophy; bone marrow;
KW osteoporosis; cancer; autoimmune disease.

OS Homo sapiens.

PN WO200176532-A2.

PD 18-OCT-2001.

PF 09-APR-2001; 2001WO-US011655.

PR 11-APR-2000; 2000US-00547596.

PA (COGE-) COGENT NEUROSCIENCE INC.

PI Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC;

DR WPI; 2002-017408/02.

DR N-PSDB; AAS63066.

PT Novel nucleic acids referred as protective sequences and their encoded
PT products for diagnosing, treating diseases involving cell death,
PT including neurological disorders e.g. stroke and for identifying
PT modulators.

PS Claim 17; Fig 8R; 256pp; English.

XX The invention relates to isolated protective sequence polypeptides (I)
CC and polynucleotides (II). (II) is useful for transferring a protective
CC sequence into a cell, which delays and/or prevents the cell from
CC undergoing cell death. Protective sequences, their products or antibodies
CC are useful diagnostically, prophylactically, therapeutically or as
CC targets for treatment and diagnosis of conditions, disorders or diseases
CC involving cell death. The protective sequences and their products are
CC useful for preventing or treating disorders of the central nervous system
CC including neurological and psychiatric conditions, cerebral oedema,
CC infections such as meningitis, degenerative diseases such as Alzheimer's
CC and motor neuron disease, demyelinating diseases such as multiple
CC sclerosis, nutritional conditions, disorders of the peripheral nervous
CC system including diabetic neuropathy, disorders which cause cell death in
CC organ systems including blood vessels, heart (ischaemia), blood cells
CC (autoimmune haemolytic anaemia), respiratory system (asthma), oral
CC cavity, gastrointestinal tract, liver (cirrhosis), pancreatitis,
CC polycystic renal disease, urinary tract, genitalia (congenital
CC anomalies), endometriosis, breast (chronic mastitis), thyroid gland
CC (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis),
CC musculoskeletal system (muscular atrophy), bone marrow or bone

CC (osteoporosis). The compositions promote cell death and are useful for
CC treating and/or ameliorating cancer and autoimmune diseases. The
CC compounds are further useful for treating physiological impacts on organs
CC caused by infection which induce cell death. (1) is useful to raise an
CC immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as markers for
CC tissues in which the corresponding protein is expressed and to isolate
CC receptors or ligands. AAU69571-AAU69736 represent the protective
CC polypeptide sequences as described in the invention

XX SQ Sequence 13 AA;

Query Match 58.0%; Score 29; DB 5; Length 13;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPDENFK 8
|||:|
Db 3 FPDENVK 9

RESULT 21

ABP46673
ID ABP46673 standard; peptide; 14 AA.

XX AC ABP46673;

DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv VH CDR3 SEQ ID 2684.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PS Claim 2; Page 3032; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX SQ Sequence 14 AA;

Query Match 58.0%; Score 29; DB 5; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
|||:|
Db 7 FPDHSEDL 14

RESULT 22

ABP46426
ID ABP46426 standard; peptide; 14 AA.

XX AC ABP46426;

DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv VH CDR3 SEQ ID 2437.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PS Claim 2; Page 2990; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX
SQ Sequence 14 AA;

Query Match 58.0%; Score 29; DB 5; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFKL 9
|||:|
Db 7 FPQESFSL 14

RESULT 23
ABU42183
ID ABU42183 standard; peptide; 9 AA.

XX
AC ABU42183;

DT 17-OCT-2003 (first entry)

DE 151P3D4 cancer gene related HLA peptide #3.

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.

XX
OS Homo sapiens.

PN WO200283860-A2.

PD 24-OCT-2002.

PF 09-APR-2002; 2002WO-US011644.

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX
PA (AGEN-) AGENSYS INC.

XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

PI Morrison RK, Ge W, Jakobovits A;

DR WPI; 2003-167091/16.

XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.

XX
PS Claim 13; Page 159; 426pp; English.

XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention

XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFKL 9
|||:|
Db 1 FPDKGHKL 8

RESULT 24
ABU41418

ID ABU41418 standard; peptide; 9 AA.

XX
AC ABU41418;

DT 17-OCT-2003 (first entry)

DE 151P3D4 cancer gene related peptide #2045.

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma.

XX
OS Unidentified.

PN WO200283860-A2.

PD 24-OCT-2002.

PF 09-APR-2002; 2002WO-US011644.

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX
PA (AGEN-) AGENSYS INC.

XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

PI Morrison RK, Ge W, Jakobovits A;

DR WPI; 2003-167091/16.

XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.

XX
PS Claim 13; Page 147; 426pp; English.

XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC 151P3D4 related peptide of the invention

XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFKL 9
|||:|
Db 2 FPDKGHKL 9

RESULT 25

ABU44334
ID ABU44334 standard; peptide; 9 AA.

XX

AC ABJ44334;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #2154.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 179; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;
XX
Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 FPDENPKL 9
|||: ||
DB 1 FPDKKHKL 8
XX
RESULT 26
ABJ45672
ID ABJ45672 standard; peptide; 9 AA.
XX
AC ABJ45672;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #3492.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX

XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 192; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;
XX
Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 FPDENPKL 9
|||: ||
DB 2 FPDKKHKL 9
XX
RESULT 27
ABJ47747
ID ABJ47747 standard; peptide; 9 AA.
XX
AC ABJ47747;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #5567.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX

XX
PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 212; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
|||: ||
Db 2 FPDKKHKL 9

RESULT 28
ABJ49116
ID ABJ49116 standard; peptide; 9 AA.
XX
AC ABJ49116;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #6936.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX

PS Claim 13; Page 225; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
|||: ||
Db 1 FPDKKHKL 8

RESULT 29
ABJ41779
ID ABJ41779 standard; peptide; 9 AA.
XX
AC ABJ41779;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related peptide #2406.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma.
XX
OS Unidentified.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 151; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a

CC 151P3D4 related peptide of the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
|||: ||
Db 1 FPDKKHKL 8

RESULT 30

ABJ41872
ID ABJ41872 standard; peptide; 9 AA.

XX AC ABJ41872;

XX DT 17-OCT-2003 (first entry)

XX DE 151P3D4 cancer gene related peptide #2499.

XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;

XX KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;

XX KW bronchial; breast; carcinoma.

XX OS Unidentified.

XX PN WO200283860-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011644.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

XX PI Morrison RK, Ge W, Jakobovits A;

XX DR WPI; 2003-167091/16.

XX PT New 151P3D4 proteins and genes, useful for eliciting a humoral or

XX PT cellular immune response, or for diagnosing, prognosing, preventing or

XX PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer

XX PS Claim 13; Page 151; 426pp; English.

XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX CC a molecule that is modulated by the 151P3D4 protein, where the status of
XX CC a cell that expresses the 151P3D4 protein is modulated. The novel
XX CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX CC a humoral or cellular immune response. The 151P3D4 genes and proteins
XX CC are also useful for diagnosing, prognosing, preventing or treating
XX CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX CC 151P3D4 related peptide of the invention

XX SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
|||: ||
Db 2 FPDKKHKL 9

RESULT 31

ABJ47004
ID ABJ47004 standard; peptide; 9 AA.

XX AC ABJ47004;

XX DT 16-OCT-2003 (first entry)

XX DE 151P3D4 cancer gene related HLA peptide #4824.

XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;

XX KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;

XX KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.

XX OS Homo sapiens.

XX PN WO200283860-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011644.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

XX PI Morrison RK, Ge W, Jakobovits A;

XX DR WPI; 2003-167091/16.

XX PT New 151P3D4 proteins and genes, useful for eliciting a humoral or

XX PT cellular immune response, or for diagnosing, prognosing, preventing or

XX PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer

XX PS Claim 13; Page 205; 426pp; English.

XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX CC a molecule that is modulated by the 151P3D4 protein, where the status of
XX CC a cell that expresses the 151P3D4 protein is modulated. The novel
XX CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX CC a humoral or cellular immune response. The 151P3D4 genes and proteins
XX CC are also useful for diagnosing, prognosing, preventing or treating
XX CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX CC human leukocyte antigen peptide relating to the 151P3D4 composition of
XX CC the invention

XX SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
|||: ||
Db 2 FPDKKHKL 9

RESULT 32

ABJ39404
ID ABJ39404 standard; peptide; 9 AA.

XX AC ABJ39404;

XX DT 17-OCT-2003 (first entry)

XX DE 151P3D4 cancer gene related peptide #31.

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma.
XX
OS Unidentified.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
XX WPI; 2003-167091/16.
DR
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
XX
PS Claim 13; Page 127; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC 151P3D4 related peptide of the invention
XX
SQ Sequence 9 AA;
QY
DB 2 FPDENFKL 9
1 FPDKKHKL 8
RESULT 33
ABJ44281
ID ABJ44281 standard; peptide; 9 AA.
XX
AC ABJ44281;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #2101.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX

PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
XX WPI; 2003-167091/16.
DR
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
XX
PS Claim 13; Page 179; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;
QY
DB 2 FPDENFKL 9
2 FPDKKHKL 9
RESULT 34
ABJ45005
ID ABJ45005 standard; peptide; 9 AA.
XX
AC ABJ45005;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #2825.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
XX WPI; 2003-167091/16.
DR
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or

PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 186; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFKL 9
Db 1 FPDKKHKL 8

RESULT 35
ABJ45032
ID ABJ45032 standard; peptide; 9 AA.
XX
AC ABJ45032;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #2852.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 186; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting

CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FPDENFKL 9
Db 2 FPDKKHKL 9

RESULT 36
ABJ48393
ID ABJ48393 standard; peptide; 9 AA.
XX
AC ABJ48393;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #6213.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 218; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;